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STIC Search Report

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STIC Database Tracking Number: 94602

TO: Dong Jiang
Location: CM1-10D19
Art Unit: 1646
Thursday, May 22, 2003

Case Serial Number: 09/036434

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
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Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Elapsed time: _____	_____ Pre-S	_____ Dialog
CPU time: _____	Type of Search	_____ APS
Total time: <u>23</u>	_____ N.A. Sequence	_____ Geninfo
Number of Searches: _____	_____ A.A. Sequence	_____ SDC
Number of Databases: <u>1</u>	_____ Structure	_____ DARC/Questel
	_____ Bibliographic	✓ Other <u>CGN</u>

GenCore version 5.1.4.p5-4572
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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:08:42 ; Search time 35 seconds
(without alignments):
60.915 Million cells updates/sec

Title: US-10-036-434-1

Perfect score: 88

Sequence: 1 DSVCPQKYLHPQXNS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 9 (8473)

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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19: /SID22/gcgdata/geneseq/geneseq-emb1/AA2008.DAT*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA2009.DAT*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2010.DAT*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2011.DAT*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2012.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	86	97.7	16 10 AAP90862	Amino acid sequence
2	86	97.7	18 20 AAW83557	Tumour necrosis fa
3	86	97.7	28 12 AAR11072	Peptide fragment #
4	86	97.7	28 20 AAY30924	Human tumour necro
5	86	97.7	28 22 AAB86808	Human TNF binding
6	86	97.7	102 12 AAR10984	Partial sequence 3
7	86	97.7	102 22 AAB37674	Human 30 kDa TNF i
8	86	97.7	106 19 AAW52273	Truncated stNFR pr
9	86	97.7	106 19 AAW52275	Truncated stNFR pr
10	86	97.7	106 20 AAW89235	Protein SEQ ID NO:

11	86	97.7	109	19	AAW52274	Truncated stNFR pr
12	86	97.7	109	20	AAW89236	Protein SEQ ID NO:
13	86	97.7	109	20	AAW89237	Protein SEQ ID NO:
14	86	97.7	110	19	AAW52268	Truncated soluble
15	86	97.7	125	22	AAB37675	Human 30 kDa TNF i
16	86	97.7	143	22	AAB37673	Human 30 kDa TNF i
17	86	97.7	154	13	AAR24082	Truncated TNF-alpha
18	86	97.7	159	13	AAR24083	Truncated TNF-alpha
19	86	97.7	161	13	AAR27496	Native 30 kD TNF i
20	86	97.7	161	19	AAW59664	Human soluble tumo
21	86	97.7	161	19	AAW52267	Soluble tumour nec
22	86	97.7	161	20	AAW89233	Tumour necrosis in
23	86	97.7	161	22	AAB37676	Human 30 kDa TNF i
24	86	97.7	162	23	AAW80508	Human TNFR1 extrac
25	86	97.7	168	13	AAR24084	Truncated TNF-alpha
26	86	97.7	199	13	AAR24080	Truncated TNF-alpha
27	86	97.7	211	20	AAW89225	Tumour necrosis fa
28	86	97.7	256	18	AAW33357	TBP(20-161)/hCG-al
29	86	97.7	280	22	AAW66979	Tnfr1 protein
30	86	97.7	285	18	AAW33359	TBP(20-190)/hCG-al
31	86	97.7	307	18	AAW33358	TBP(20-161)/hCG-be
32	86	97.7	309	16	AAW70108	TNF-R-GBPH fusion
33	86	97.7	311	20	AAW89229	Tumour necrosis fa
34	86	97.7	336	18	AAW33360	TBP(20-190)/hCG-be
35	86	97.7	366	20	AAW89228	Tumour necrosis fa
36	86	97.7	371	11	AAW07449	Tumour Necrosis Fa
37	86	97.7	397	20	AAW89227	Tumour necrosis fa
38	86	97.7	417	20	AAW89226	Tumour necrosis fa
39	86	97.7	420	20	AAW89224	Tumour necrosis fa
40	86	97.7	433	14	AAW51032	Mutant p55 tumour
41	86	97.7	443	14	AAW51033	Mutant p55 tumour
42	86	97.7	451	16	AAW70107	TNF-R-GBP 130 fusi
43	86	97.7	455	11	AAW07451	Human Tumour Necro
44	86	97.7	455	12	AAW10986	30kD TNF inhibitor
45	86	97.7	455	12	AAR11082	Human 55kD TNF-bin

ALIGNMENTS

RESULT 1
AAP90862
10 AAP90862 standard; protein; 16 AA.
XX AAP90862;
AC AAP90862;
XX
DT 03-OCT-2002 (updated)
DT 23-JUN-1990 (first entry)
XX
DE Amino acid sequence of N-terminus of tumour necrosis factor (TNF)
DE Inhibitory protein.
XX
KW Tumour necrosis factor inhibitory protein; TNF.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 4
FT /note="The identification of this residue is theoretical"
XX
PN EP308378-A.
XX
PD 22-MAR-1989.
XX
XX 13-SEP-1988; 88EP-0830365.
XX
PR 13-SEP-1987; 87IL-0083878.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Wallach D, Engelmann H, Aderka D, Rubinstein M;
XX WPI; 1989-097746/12.
DR

XX Tumour Necrosis Factor Inhibitory protein -
PT isolated from urine and having ability to inhibit the binding of
PT TNF to its receptors and its cytotoxic effect
XX
XX Claim 8: page 12; 19pp; English.
XX
XX TNF inhibitory protein is pref isolated from human urine. This sequence
CC is claimed as are TNF inhibitory protein, its salts and functional
CC deriva. and active fractions which have the ability to inhibit the
CC binding of TNF to its receptors; and the cytotoxic effect of TNF. TNF
CC inhibitory protein can be used for antagonising the deleterious effects
CC of TNF in mammals, eg for treating conditions where there is an
CC over-prodn. of endogenous TNF, such as in cases of septic shock,
CC rheumatoid arthritis. It can also be used in cases of exogenous admin.
CC of excessive amts. of TNF. Purified TNF inhibitory protein is produced by
CC purification from the crude protein fraction from a dialysed concentrate of
CC human urine.
CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
XX
XX Sequence 16 AA;
XX
XX
XX Query Match 97.7%; Score 86; DB 10; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 DSVCPQCKYIHPOXNS 16
XX | | | | | | | | | | | | | | | |
XX Db 1 DSVCPQCKYIHPOXNS 16
XX
XX
XX RESULT 2
XX AAW83557
XX ID AAW83557 standard; peptide: 18 AA.
XX AC AAW83557;
XX XX
XX DT 04-MAR-1999 (first entry)
XX DE Tumour necrosis factor receptor N-terminal peptide #15.
XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor: osteoprotegerin;
XX OP; chimeric; fusion; dimerisation domain; autoimmune disease.
XX KW Inflammation; apoptosis.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO9849305-A1.
XX XX
XX PD 05-NOV-1998.
XX XX
XX PF 29-APR-1998; 98WO-US08631.
XX XX
XX PR 01-MAY-1997; 97US-0850188.
XX XX
XX PA (AMGE-) AMGEN INC.
XX XX
XX PI Boyle WJ, Wooden S;
XX XX
XX DR WPI: 1999-034661/03.
XX XX
XX New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
XX PS Disclosure: Page 16; 92pp; English.
XX XX
XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid

CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNF N-terminal peptide from
CC the present invention.
XX
XX Sequence 18 AA;
XX
XX Query Match 97.7%; Score 86; DB 20; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.5e-07;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 DSVCPQCKYIHPOXNS 16
XX | | | | | | | | | | | | | | | |
XX Db 1 DSVCPQCKYIHPOXNS 16
XX
XX
XX RESULT 3
XX AAR11072
XX ID AAR11072 standard; peptide: 28 AA.
XX AC AAR11072;
XX XX
XX DT 24-MAY-1991 (first entry)
XX XX
XX DE Peptide fragment #1 of 55KD TNF-binding protein.
XX KW Tumour Necrosis Factor; binding proteins; septic shock;
XX KW autoimmune glomerulonephritis; lymphokine; cytokine.
XX XX
XX PN EP417563-A.
XX XX
XX PD 20-MAR-1991.
XX XX
XX PF 31-AUG-1990; 90EP-0116707.
XX XX
XX PR 20-APR-1990; 90CH-0001347.
XX PR 12-SEP-1989; 89CH-0003319.
XX PR 08-MAR-1990; 90CH-0000746.
XX XX
XX PA (HOFF) HOFFMANN-LA ROCHE AG.
XX XX
XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
XX PI Schlaeger EJ;
XX XX
XX DR WPI: 1991-081851/12.
XX XX
XX PT Insoluble tumour necrosis factor binding proteins - and DNA
XX PT encoding them, useful in pharmaceutical prods. and for antibody
XX PT prodn.
XX XX
XX PS Claim 3: Page 19; 26pp; German.
XX XX
XX Cells which produce TNF-binding proteins (-BP)(eg HL60 cells) were
CC cultured and the supernatant centrifuged, put on a column of
CC "Affigel 10" to which recombinant TNF-alpha was bonded, and TNF-BP
CC eluted. The recovered protein was used as an immunogen to raise
CC monoclonal antibodies. The MAb's were attached to Sepharose 4B and
CC cell extract purified on a system of: BSA-Sepharose 4B; AU-Sepharose-
CC 4B and TNF alpha-Sepharose 4B. Active TNF-BP were eluted from the
CC last two columns and separated by gel electrophoresis to identify
CC bands of mol. wt.s 75, 65, 55, 51, 38, 36 and 34KD. Partial amino
CC acid sequences were determined for the 75 and 55KD proteins,
CC including the fragment given here which is a minimum sequence for
CC TNF-binding.
CC See also AAR11073-K11081 and AAR10955-6.
XX

SQ Sequence 28 AA:

Query Match 97.7%; Score 86; DB 12; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSVCPQCKYIHPQXNS 16
 |||||
 Db 12 DSVCPQCKYIHPQXNS 27

RESULT 4

AAAY30924
 ID AAY30924 standard; peptide; 28 AA.

AC AAY30924;

DT 18-OCT-1999 (first entry)

XX Human tumour necrosis factor binding protein fragment 1A.

XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
 KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
 KW autoimmune glomerulonephritis; cerebral malaria; immune response;
 KW antagonist; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 25

FT /label= unknown

XX EP939121-A2.

XX 01-SEP-1999.

XX 31-AUG-1990; 90EP-0116707.

XX 20-APR-1990; 90CH-0001347.

XX 12-SEP-1989; 89CH-0003319.

XX 08-MAR-1990; 90CH-0000746.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

XX Schlaeager E;

XX WPI; 1999-480840/41.

XX New insoluble proteins, and fragments, that bind to tumour necrosis

XX factor, used to treat e.g. septic shock or cerebral malaria

XX Claim 3; Page 2; 25pp; German.

XX This invention describes novel homogeneous insoluble proteins (I),

XX their (insoluble) fragments (Ia) and their salts that can bind tumour

XX necrosis factor (TNF). The products of the invention have

XX anti-inflammatory and antimalarial activity (i) and (ii) are used (i)

XX to treat diseases in which TNF is involved (e.g. septic shock,

XX autoimmune glomerulonephritis, cerebral malaria, immune responses and

XX inflammation), (ii) to purify TNF, (iii) to identify TNF antagonists

XX and (iv) for diagnostic determination of TNF in body fluids. Antibodies

XX raised against (I) are used for affinity purification of (I).

XX AAAY30924-Y30933 represent fragments of the tumour necrosis factor

XX described in the invention.

XX Sequence 28 AA:

Db 12 DSVCPQCKYIHPQXNS 27

RESULT 5

AAAB86808

ID AAB86808 standard; peptide; 28 AA.

AC AAB86808;

DT 12-NOV-2001 (first entry)

XX Human TNF binding protein fragment 1A.

XX Human; TNF; tumor necrosis factor binding protein; TNFBP; treatment;
 KW insoluble protein; anti-inflammatory; immunosuppressive; antibacterial;
 KW antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
 KW autoimmune glomerulonephritis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 25

FT /label= OTHER

FT /note= "unidentified residue"

XX EP1132471-A2.

XX 12-SEP-2001.

XX 31-AUG-1990; 2001EP-0108117.

XX 12-SEP-1989; 89CH-0003319.

XX 08-MAR-1990; 90CH-0000746.

XX 20-APR-1990; 90CH-0001347.

XX 31-AUG-1990; 90EP-0116707.

XX 31-AUG-1990; 99EP-0100703.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

XX Schlaeager E;

XX WPI; 2001-559312/63.

XX New homogeneous, insoluble proteins that bind tumor necrosis factor

XX (TNF), useful for treating TNF-mediated disorders, e.g. inflammation

XX Claim 3; Page 2; 26pp; German.

XX This invention describes novel insoluble proteins (I), also their

XX (insoluble) fragments and pharmaceutically acceptable salts, able to bind

XX tumor necrosis factor (TNF) and in homogeneous form. The products of the

XX invention have antiinflammatory, immunosuppressive, antibacterial,

XX antiprotozoal activity. (i), and related recombinant proteins, are used

XX to treat diseases mediated by TNF, e.g. shock in cases of meningococcal

XX sepsis; development of autoimmune glomerulonephritis and cerebral

XX malaria. Also (i), or antibodies specific for them, are used for

XX diagnostic determination of TNF in body fluids, for affinity purification

XX of TNF and for identifying (antagonists of TNF. This sequence represents

XX a tumor necrosis factor binding protein fragment 1A which is used to

XX illustrate the method of the invention.

XX Sequence 28 AA:

Query Match 97.7%; Score 86; DB 22; Length 28;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSVCPQCKYIHPQXNS 16

Db 12 DSVCPQCKYIHPQXNS 27

RESULT 6

AA010984
ID AAR10984 standard; Protein; 102 AA.
XX
AC AAR10984;
XX
DT 13-MAY-1991 (first entry)
XX
DE Partial sequence 30kd TNF inhibitor.
XX
KW Tumour necrosis factor; inhibitor.
XX
OS Homo sapiens.
FH Key
FT Region 1..52 Location/Qualifiers
FT /label= exon I
FT Region 53..95
FT /label= exon II
FT Region 96..102
FT /label= exon III
FT /note= "incomplete"

XX AU9058976-A.

XX 24-JAN-1991.

XX 16-JUL-1990; 90AU-0058976.

XX 07-FEB-1990; 90US-0479661.

XX 18-JUL-1989; 89US-0381080.

XX 11-DEC-1989; 89US-0450329.

XX (SYNE-) SYNERGEN INC.

XX WPI; 1991-073847/11.

XX N-PSDB; AAQ10878.

XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha

XX and -beta, useful as therapeutic agent.

XX Disclosure; Fig 13; 142pp; English.

XX The sequence comprises 48 residues of the 30 kD TNF inhibitor glycoprotein, in three exons. The clone from which the sequence was obt'd. was isolated from a human genomic library. The clone gene can be inserted into expression vectors for prep'n of TNF inhibitor for use in the treatment of inflammatory and degenerative diseases.

XX See also AAR10986 and AAR11001.

XX Sequence 102 AA;

Query Match 97.7%; Score 86; DB 12; Length 102;

Best Local Similarity 93.8%; Pred. No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPOXNS 16

DB 28 DSVCPQCKYIHPOXNS 43

RESULT 7

AA037674
ID AAB37674 standard; protein; 102 AA.
XX
AC AAB37674;

XX 02-MAR-2001 (first entry)

XX Human 30 kDa TNF inhibitor fragment #2.

XX

TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; Interleukin; IL-1; inflammatory disease; degenerative disease; human.

OS Homo sapiens.

PN US6143866-A.

XX 07-NOV-2000.

XX 19-JAN-1995; 95US-0375242.

XX 19-JUL-1990; 90US-0555274.

XX 09-JUL-1993; 93US-0090366.

XX 18-JUL-1989; 89US-0381080.

XX 11-DEC-1989; 89US-0450329.

XX 07-FEB-1990; 90US-0479661.

XX (AMGE-) AMGEN INC.

XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;

PI Vanderslice RW, Vannice J, Kohno T;

XX WPI; 2001-006443/01.

XX N-PSDB; AAC83944.

Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by TNF

Example 5; Fig 13; 82pp; English.

XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is a fragment of the 30 kDa TNF inhibitor (AAB37676). The 30 kDa TNF inhibitor can inhibit TNF alpha.

XX Sequence 102 AA;

Query Match 97.7%; Score 86; DB 22; Length 102;

Best Local Similarity 93.8%; Pred. No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 DSVCPQCKYIHPOXNS 16

DB 28 DSVCPQCKYIHPOXNS 43

RESULT 8

AAW52273

ID AAW52273 standard; Protein; 106 AA.

XX AAW52273;

XX 29-JUN-1998 (first entry)

XX Truncated stNFR protein, stNFR-I 2.6D/C105.

XX Soluble tumour necrosis factor receptor; stNFR; TNF-mediated disease; tumour necrosis factor binding protein; autoimmune disease; arthritis; adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy; chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.

XX Homo sapiens.

XX WO9801555-A2.

XX 15-JAN-1998.

XX 09-JUL-1997; 97WO-US12244.

```
XX 04-MAR-1997; 97US-0039792.
PR 09-JUL-1996; 96US-0021443.
PR 06-DEC-1996; 96US-0032534.
PR 23-JAN-1997; 97US-0037737.
PR 07-FEB-1997; 97US-0039314.
XX (AMGE-) AMGEN INC.
PA Edwards CK, Fisher EF, Kieft GL;
XX WPI: 1998-101052/09.
XX N-PSDB: AAV19803.
XX Truncated and soluble forms of tumour necrosis factor receptor -
PT useful for treating diseases involving factor, e.g. arthritis and
PT adult respiratory distress syndrome
XX Claim 2; Fig 2; 205pp; English.
XX This sequence is a truncated human soluble tumour necrosis factor
CC receptor (sTNFR) protein of the invention. The protein is designated
CC sTNFR-I 2.6D/C105. The truncated sTNFR proteins and tumour necrosis
CC factor binding proteins (TNBP) are used to treat any TNF-mediated
CC disease, e.g. arthritis, adult respiratory distress syndrome,
CC cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection,
CC Alzheimer's disease and other autoimmune diseases. Cells transformed with
CC a vector containing DNA encoding the protein may be used for production
CC of recombinant sTNFR, which may also be used for measuring the amount of
CC sTNFR in samples and to raise antibodies against sTNFR. TNBP may also be
CC used in preparation of therapeutic compositions for treating the above
CC diseases. The sTNFR proteins are well suited to large scale production
CC (since they lack the deamidation site in region 111-126, so are more
CC stable in vivo); contain fewer disulphide bonds and fewer epitopes,
CC making them less antigenic than full-length proteins.
XX Sequence 106 AA;
SQ Query Match 97.7%; Score 86; DB 19; Length 106;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGGKYIHPQXNS 16
Db | | | | | | | | | | | | | | | | |
2 DSVCPQGGKYIHPQNNNS 17

RESULT 9
AAW52275
ID AAW52275 standard; Protein; 106 AA.
XX AC AAW52275;
XX DT 29-JUN-1998 (first entry)
XX DE Truncated sTNFR protein, sTNFR-I 2.6D/N105.
XX KW Soluble tumour necrosis factor receptor; sTNFR; TNF-related disease;
XX KW tumour necrosis factor binding protein; autoimmune disease arthritis;
XX KW adult respiratory distress syndrome; cachexia/anorexia; cancer therapy;
XX KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.
XX OS Homo sapiens.
XX PN W09801555-A2.
XX PD 15-JAN-1998.
XX PF 09-JUL-1997; 97W0-US12244.
XX PR 04-MAR-1997; 97US-0039792.
XX PR 09-JUL-1996; 96US-0021443.
XX PR 06-DEC-1996; 96US-0032534.
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PR 23-JAN-1997; 97US-0037737.
PR 07-FEB-1997; 97US-0039314.
XX (AMGE-) AMGEN INC.
XX Edwards CK, Fisher EF, Kieft GL;
XX WPI: 1998-101052/09.
XX N-PSDB: AAV19805.
XX Truncated and soluble forms of tumour necrosis factor receptor -
PT useful for treating diseases involving factor, e.g. arthritis and
PT adult respiratory distress syndrome
XX Claim 2; Fig 4; 205pp; English.
XX This sequence is a truncated human soluble tumour necrosis factor
CC receptor (sTNFR) protein of the invention. The protein is designated
CC sTNFR-I 2.6D/N105. The truncated sTNFR proteins and tumour necrosis
CC factor binding proteins (TNBP) are used to treat any TNF-mediated
CC disease, e.g. arthritis, adult respiratory distress syndrome,
CC cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection,
CC Alzheimer's disease and other autoimmune diseases. Cells transformed with
CC a vector containing DNA encoding the protein may be used for production
CC of recombinant sTNFR, which may also be used for measuring the amount of
CC sTNFR in samples and to raise antibodies against sTNFR. TNBP may also be
CC used in preparation of therapeutic compositions for treating the above
CC diseases. The sTNFR proteins are well suited to large scale production
CC (since they lack the deamidation site in region 111-126, so are more
CC stable in vivo); contain fewer disulphide bonds and fewer epitopes,
CC making them less antigenic than full-length proteins.
XX Sequence 106 AA;
SQ Query Match 97.7%; Score 86; DB 19; Length 106;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGGKYIHPQXNS 16
Db | | | | | | | | | | | | | | | | |
2 DSVCPQGGKYIHPQNNNS 17

RESULT 10
AAW89235
ID AAW89235 standard; Protein; 106 AA.
XX AC AAW89235;
XX DT 04-MAR-1999 (first entry)
XX DE Protein SEQ ID NO:82 from W09849305.
XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
XX KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
XX KW inflammation; apoptosis.
XX OS Unidentified.
XX PN W09849305-A1.
XX PD 05-NOV-1998.
XX PF 29-APR-1998; 98W0-US08631.
XX PR 01-MAY-1997; 97US-0850188.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Wooden S;
XX PR 1999-034661/03.
XX DR WPI: 1999-034661/03.
XX
```


CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a protein given in the sequence
CC listing but not mentioned further within the specification.

```

SQ      Sequence      109 AA;
Query Match      97.7%; Score 86; DB 19; Length 109;
Best Local Similarity 93.8%;
Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DSVCPQGGKYIHPPQXNS 16
          |||||
Db       2 DSVCPQGGKYIHPPQNS 17
          |||||

```

RESULT 12
AAW89236
ID AAW89236 standard; Protein; 109 AA.
XX
XX AAW89236;
XX
XX
XX 04-MAR-1999 (first entry)
XX
XX
XX Protein SEQ ID NO:83 from W09849305.
XX
XX
XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.

XX Unidentified.
OS
XX
XX WO9849305-A1.
PN
XX
XX 05-NOV-1998.
PD
XX
XX
PF 29-APR-1998; 98WO-US08631.
XX
XX
PR 01-MAY-1997; 97US-0850188.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX
PI Boyle WJ, Wooden S;
XX
XX WPI; 1999-034661/03.
DR
XX
XX New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
XX Disclosure; Page 74; 92pp; English.
PS

xx The present invention describes a chimeric polypeptide (A1), comprising
CC an osteopontin (OPN) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products

CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a protein given in the sequence
CC listing but not mentioned further within the specification.

XX Sequence 109 AA;

Query Match 97.7%; Score 86; DB 20; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
IIIIIIIIIIII II
Db 2 DSVCPQGYIHPQXNS 17

RESULT 13

AAW89237
ID AAW89237 standard; Protein: 109 AA.

XX AAW89237;

XX 04-MAR-1999 (first entry)

DE Protein SEQ ID NO:84 from WO9849305.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW Inflammation; apoptosis.

XX Unidentified.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0050188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI: 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders

XX Disclosure: Page 74-75: 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressed. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a protein given in the sequence
CC listing but not mentioned further within the specification

XX Sequence 109 AA;

Query Match 97.7%; Score 86; DB 20; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
IIIIIIIIIIII II
Db 2 DSVCPQGYIHPQXNS 17

RESULT 14
AAW52268
ID AAW52268 standard; Protein: 110 AA.

XX AAW52268;

XX 29-JUN-1998 (first entry)

DE Truncated soluble tumour necrosis factor receptor.

XX Soluble tumour necrosis factor receptor; TNFR: "TNF-mediated disease;
KW tumour necrosis factor binding protein; autoimmune disease; arthritis;
KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;
KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..18 /note= "optionally deleted"

FT Misc-difference 19..103

FT Misc-difference 104..110 /note= "residues 19-103 of human TNFR"

FT Misc-difference 104..110 /note= "optionally deleted"

XX WO9801555-A2.

XX 15-JAN-1998.

XX 09-JUL-1997; 97WO-US12244.

XX 04-MAR-1997; 97US-0039792.

XX 09-JUL-1996; 96US-0021443.

XX 06-DEC-1996; 96US-0032534.

XX 23-JAN-1997; 97US-0037737.

XX 07-FEB-1997; 97US-0039314.

XX (AMGE-) AMGEN INC.

XX Edwards CK, Fisher EF, Kieft GL;

XX WPI: 1998-101052/09.

XX Truncated and soluble forms of tumour necrosis factor receptor -
PT useful for treating diseases involving factor, e.g. arthritis and
PT adult respiratory distress syndrome

XX Claim 1; Page -: 205pp; English.

XX This sequence is a truncated soluble tumour necrosis factor receptor
CC (TNFR) protein of the invention. The truncated TNFR proteins and tumour
CC necrosis factor binding proteins (TNBP) are used to treat any
CC TNF-mediated disease, e.g. arthritis, adult respiratory distress
CC syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft
CC rejection, Alzheimer's disease and other autoimmune diseases. Cells
CC transformed with a vector containing DNA encoding the protein may be used
CC for production of recombinant TNFR, which may also be used for measuring
CC the amount of TNFR in samples and to raise antibodies against TNFR.
CC TNBP may also be used in preparation of therapeutic compositions for
CC treating the above diseases. The TNFR proteins are well suited to large
CC scale production (since they lack the dimerisation site in region 111-126,

CC so are more stable in vivo); contain fewer disulphide bonds and fewer
CC epitopes, making them less antigenic than full-length proteins.

XX Sequence 110 AA;

Query Match 97.7%; Score 86; DB 15; Length 125;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQCKYIHPQXNS 16
| | | | | | | | | | | | | | | |
Db 1 DSVCPQCKYIHPQXNS 16

RESULT 15

AAB37675
ID AAB37675 standard; protein; 125 AA.

XX AC AAB37675;

XX DT 02-MAR-2001 (first entry)

XX DE Human 30 kDa TNF inhibitor fragment #3.

XX KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
XX IL-1; inflammatory disease; degenerative disease; human.

XX OS Homo sapiens.

XX PN US6143866-A.

XX PD 07-NOV-2000.

XX PF 19-JAN-1995; 95US-0375242.

XX PR 19-JUL-1990; 90US-0555274.

XX PR 09-JUL-1993; 93US-0090366.

XX PR 18-JUL-1989; 89US-0381080.

XX PR 11-DEC-1989; 89US-0450329.

XX PR 07-FEB-1990; 90US-0479601.

XX PA (AMGE-) AMGEN INC.

XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RE;

XX PI Vanderslice RW, Vannice J, Kohno T;

XX DR WPI; 2001-006443/01.

XX PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF -

XX PS Disclosure; Fig 14; 82pp; English.

XX CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is a fragment of the 30 kDa TNF inhibitor (AAB37676).
CC The 30 kDa TNF inhibitor can inhibit TNF alpha.

XX S0 Sequence 125 AA;

Query Match 97.7%; Score 86; DB 22; Length 125;
Best Local Similarity 93.8%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQCKYIHPQXNS 16
| | | | | | | | | | | | | | | |
Db 1 DSVCPQCKYIHPQXNS 16

Search completed: May 21, 2003, 18:25:52
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:25:22 ; Search time 15 seconds
(without alignments)
31.384 Million cell updates/sec

Title: US-10-036-434-1

Perfect score: 88
Sequence: 1 DSVCPQGYHPQXNS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	97.7	16	1	US-07-879-373-1
2	86	97.7	153	1	US-08-050-319B-52
3	86	97.7	153	2	US-08-465-982-52
4	86	97.7	158	1	US-08-050-319B-54
5	86	97.7	158	2	US-08-465-982-54
6	86	97.7	161	4	US-09-326-394-2
7	86	97.7	167	1	US-08-050-319B-2
8	86	97.7	167	1	US-08-050-319B-57
9	86	97.7	167	2	US-08-465-982-2
10	86	97.7	167	2	US-08-465-982-57
11	86	97.7	197	4	US-08-828-683A-21
12	86	97.7	256	4	US-08-804-166-2
13	86	97.7	256	4	US-08-910-991-2
14	86	97.7	280	3	US-08-974-022-46
15	86	97.7	280	4	US-08-795-445A-46
16	86	97.7	280	4	US-08-795-447A-46
17	86	97.7	280	4	US-08-974-186-46
18	86	97.7	280	4	US-08-795-446B-46
19	86	97.7	285	4	US-08-706-945D-132
20	86	97.7	285	4	US-08-804-166-6
21	86	97.7	285	4	US-08-910-991-6
22	86	97.7	307	4	US-08-804-166-4
23	86	97.7	307	4	US-08-910-991-4
24	86	97.7	336	4	US-08-804-166-4
25	86	97.7	336	4	US-08-910-991-4
26	86	97.7	455	1	US-08-050-319B-25
27	86	97.7	455	1	US-08-321-668-2

Sequence 2, Appli
Sequence 2, Appli
Sequence 25, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 4, Appli
Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-07-879-373-1
: Sequence 1, Application US/07879373
: Patent No. 5512544
: GENERAL INFORMATION:
: APPLICANT: Wallach, David
: APPLICANT: Aderka, Dan
: APPLICANT: Engelmann, Hartmut
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
: TITLE OF INVENTION: COMPRISING AN ANTICYTOKINE
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Browdy and Neimark
: STREET: 419 Seventh St., NW, Suite 300
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/879,373
: FILING DATE: 19920507
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Taruza, John E
: REGISTRATION NUMBER: 33,638
: REFERENCE/DOCKET NUMBER: Wallach6
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 16 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
US-07-879-373-1

Query Match 97.7%; Score 86; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSVCPQGYHPQXNS 16

Db 1 DSVCPQGYIHPQXNS 16
|||||

RESULT 2

US-08-050-319B-52
; Sequence 52, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050.319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-52

Query Match 97.7%; Score 86; DB 1; Length 153;
Best Local Similarity 93.8%; Pred. No. 8.4e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
|||||

Db 41 DSVCPQGYIHPQXNS 56

RESULT 3

US-08-465-982-52
; Sequence 52, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465.982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050.319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-982-52

Query Match 97.7%; Score 86; DB 2; Length 153;
Best Local Similarity 93.8%; Pred. No. 8.4e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
|||||

Db 41 DSVCPQGYIHPQXNS 56

RESULT 4

US-08-050-319B-54
; Sequence 54, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050.319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

APPLICANT: Sennello, Regina M.
APPLICANT: Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BLOCKING

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

RESULT 7
US-08-050-319B-2
: Sequence 2, Application US/08050319B
: Patent No. 5633145
: GENERAL INFORMATION:
: APPLICANT: M.Feldmann, P.W. Gray,
: APPLICANT: M.J.C. Turner, F.M. Brennan
: TITLE OF INVENTION: Modified human TNFalpha (Tumor
: TITLE OF INVENTION: Necrosis Factor alpha) Receptor
: NUMBER OF SEQUENCES: 57

```

```

: STREET: 635 Bryant Street
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94301
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Pascal in Release #1.0, version #1.25
:

```

1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050.319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-2

Query Match 97.7%; Score 86; DR 1; Length 167;
Best Local Similarity 93.8%; Pred. No. 9.2e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
|||||
Db 41 DSVCPQGYIHPQXNS 56

RESULT 8
US-08-050-319B-57
Sequence 57, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050.319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-57

Query Match 97.7%; Score 86; DB 1; Length 167;
Best Local Similarity 93.8%; Pred. No. 9.2e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
|||||
Db 41 DSVCPQGYIHPQXNS 56

RESULT 9
US-08-465-982-2
Sequence 2, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050.319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-2

Query Match 97.7%; Score 86; DB 2; Length 167;
Best Local Similarity 93.8%; Pred. No. 9.2e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
|||||
Db 41 DSVCPQGYIHPQXNS 56

RESULT 10
US-08-465-982-57
Sequence 57, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California

COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050.319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-57

Query Match 97.7%; Score 86; DB 2; Length 167;
Best Local Similarity 93.8%; Pred. No. 9.2e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
|||||
Db 41 DSVCPQGYIHPQNS 56

RESULT 11

US-08-828-683A-21
Sequence 21, Application US/08828683A
Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828.683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-828-683A-21

Query Match 97.7%; Score 86; DB 4; Length 197;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
|||||
Db 41 DSVCPQGYIHPQNS 56

RESULT 12

US-08-804-166-2
Sequence 2, Application US/08804166
Patent No. 6193972

GENERAL INFORMATION:

APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.166
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-804-166-2

Query Match 97.7%; Score 86; DB 4; Length 256;
Best Local Similarity 93.8%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQXNS 16
|||||
Db 23 DSVCPQGYIHPQNS 38

RESULT 13

US-08-910-991-2
; Sequence 2, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 828-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-910-991-2

Query Match 97.7%; Score 86; DB 4; Length 256;
Best Local Similarity 93.8%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy 1 DSVCPQCKYIHPOXNS 16
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Db 23 DSVCPQCKYIHPOXNS 38

RESULT 14
US-08-974-022-46
; Sequence 46, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-46

Query Match 97.7%; Score 86; DB 3; Length 280;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy 1 DSVCPQCKYIHPOXNS 16
| | | | | | | | | | | | | | | | | |
Db 41 DSVCPQCKYIHPOXNS 56

RESULT 15
US-08-795-445A-46
; Sequence 46, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-795-445A-46

Query Match 97.7%; Score 86; DB 4; Length 280;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
| | | | | | | | | | | | | | | |
Db 41 DSVCPQGYIHPQNNNS 56

Search completed: May 21, 2003, 18:28:25
Job time : 17 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:25:57 : Search time 17 seconds
(without alignments)
93.339 Million cell updates/sec

Title: US-10-036-434-1

Perfect score: 88
Sequence: 1 DSVCPQGYIHPOXNS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCT05_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	97.7	16	9 US-10-036-434-1	Sequence 1, Appli
2	86	97.7	16	9 US-10-036-452-1	Sequence 2, Appli
3	86	97.7	35	9 US-10-125-062-2	Sequence 2, Appli
4	86	97.7	49	9 US-10-125-062-8	Sequence 8, Appli
5	86	97.7	49	9 US-10-125-062-9	Sequence 9, Appli
6	86	97.7	69	9 US-10-125-062-3	Sequence 3, Appli
7	86	97.7	106	9 US-09-882-735-4	Sequence 4, Appli
8	86	97.7	106	9 US-09-882-735-4	Sequence 4, Appli
9	86	97.7	109	9 US-09-882-735-6	Sequence 6, Appli
10	86	97.7	161	9 US-09-898-234-4	Sequence 4, Appli
11	86	97.7	161	9 US-09-899-429A-4	Sequence 4, Appli
12	86	97.7	161	9 US-09-792-356-4	Sequence 4, Appli
13	86	97.7	161	9 US-09-882-735-2	Sequence 2, Appli
14	86	97.7	161	10 US-09-899-422-4	Sequence 4, Appli
15	86	97.7	161	10 US-09-907-263-2	Sequence 2, Appli
16	86	97.7	162	9 US-09-899-429A-6	Sequence 6, Appli
17	86	97.7	162	9 US-09-852-455-5	Sequence 5, Appli
18	86	97.7	162	10 US-09-798-789-9	Sequence 9, Appli
19	86	97.7	162	10 US-09-798-789-10	Sequence 10, Appli

20	86	97.7	162	10 US-09-798-789-11	Sequence 11, Appli
21	86	97.7	162	10 US-09-798-789-12	Sequence 12, Appli
22	86	97.7	162	10 US-09-798-789-13	Sequence 13, Appli
23	86	97.7	162	10 US-09-798-789-14	Sequence 14, Appli
24	86	97.7	162	10 US-09-798-789-15	Sequence 15, Appli
25	86	97.7	162	10 US-09-798-789-16	Sequence 16, Appli
26	86	97.7	162	10 US-09-798-789-17	Sequence 17, Appli
27	86	97.7	162	10 US-09-798-789-18	Sequence 18, Appli
28	86	97.7	162	10 US-09-798-789-19	Sequence 19, Appli
29	86	97.7	162	10 US-09-798-789-20	Sequence 20, Appli
30	86	97.7	162	10 US-09-798-789-21	Sequence 21, Appli
31	86	97.7	162	10 US-09-798-789-22	Sequence 22, Appli
32	86	97.7	172	9 US-09-899-429A-20	Sequence 20, Appli
33	86	97.7	173	9 US-09-899-429A-16	Sequence 10, Appli
34	86	97.7	183	9 US-09-899-429A-10	Sequence 10, Appli
35	86	97.7	190	9 US-09-899-429A-18	Sequence 18, Appli
36	86	97.7	197	9 US-10-112-793-21	Sequence 21, Appli
37	86	97.7	200	9 US-09-899-429A-12	Sequence 12, Appli
38	86	97.7	201	9 US-09-899-429A-14	Sequence 14, Appli
39	86	97.7	211	9 US-09-899-429A-8	Sequence 8, Appli
40	86	97.7	213	9 US-10-125-062-1	Sequence 1, Appli
41	86	97.7	256	10 US-09-756-186-2	Sequence 2, Appli
42	86	97.7	285	10 US-09-756-186-6	Sequence 6, Appli
43	86	97.7	307	10 US-09-756-186-4	Sequence 4, Appli
44	86	97.7	336	10 US-09-756-186-8	Sequence 8, Appli
45	86	97.7	371	9 US-09-898-234-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-10-036-434-1
: Sequence 1, Application US/10036434
: Patent No. US20020165163A1
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: ENGELMANN, Hartmut
: APPLICANT: ADERKA, Dan
: APPLICANT: RUBINSTEIN, Menachem
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR INHIBITORY PROTEIN AND ITS PURIFICATION
: FILE REFERENCE: WALLACHIC
: CURRENT APPLICATION NUMBER: US/10/036,434
: CURRENT FILING DATE: 2002-01-07
: PRIOR APPLICATION NUMBER: 09/414,609
: PRIOR FILING DATE: 1999-10-08
: PRIOR APPLICATION NUMBER: 08/474,691
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 07/876,828
: PRIOR FILING DATE: 1992-04-30
: PRIOR APPLICATION NUMBER: 07/243,092
: PRIOR FILING DATE: 1988-09-12
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 16
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: synthetic
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (14)..(14)
: OTHER INFORMATION: Xaa is unknown
US-10-036-434-1

Query Match 97.7%; Score 86; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPOXNS 16

|||||

Db 1 DSVCPQGYIHPOXNS 16

RESULT 2
US-10-036-452-1
; Sequence 1, Application US/10036452
; Patent No. US20020165354A1
; GENERAL INFORMATION:
; APPLICANT: WALIACH, David
; APPLICANT: ENGELMANN, Hartmut
; APPLICANT: ADERKA, Dan
; APPLICANT: RUBINSTEIN, Menachem
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR INHIBITORY PROTEIN AND ITS
; TITLE OF INVENTION: PURIFICATION
; FILE REFERENCE: WALLACHIC
; CURRENT APPLICATION NUMBER: US/10/036.452
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/414,609
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 08/474,691
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/876,828
; PRIOR FILING DATE: 1992-04-30
; PRIOR APPLICATION NUMBER: 07/243,092
; PRIOR FILING DATE: 1988-09-12
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is unknown
US-10-036-452-1

Query Match 97.7%; Score 86; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGGYIHPOXNS 16
|||||
DB 1 DSVCPQGGYIHPOXNS 16

RESULT 3
US-10-125-062-2
; Sequence 2, Application US/10125062
; Publication No. US20020192690A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Xenoport, Inc.
; TITLE OF INVENTION: Epitope-Captured Antibody Display
; FILE REFERENCE: 019282-000710US
; CURRENT APPLICATION NUMBER: US/10/125.062
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/284,305
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:sequence
; OTHER INFORMATION: displayed by T7 hTNFR-1 cDNA fragment phage clone
; OTHER INFORMATION: selected for binding to the goat anti-hTNFR
US-10-125-062-2

Query Match 97.7%; Score 86; DB 9; Length 49;

Query Match 97.7%; Score 86; DB 9; Length 35;
Best Local Similarity 93.8%; Pred. No. 1.9e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQGGYIHPOXNS 16
|||||
DB 18 DSVCPQGGYIHPOXNS 33

RESULT 4
US-10-125-062-8
; Sequence 8, Application US/10125062
; Publication No. US20020192690A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Xenoport, Inc.
; TITLE OF INVENTION: Epitope-Captured Antibody Display
; FILE REFERENCE: 019282-000710US
; CURRENT APPLICATION NUMBER: US/10/125.062
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/284,305
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:sequence
; OTHER INFORMATION: displayed by fd hTNFR-1 cDNA fragment phage clone
; OTHER INFORMATION: selected for binding to goat anti-hTNFR polyclonal
US-10-125-062-8

Query Match 97.7%; Score 86; DB 9; Length 49;
Best Local Similarity 93.8%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQGGYIHPOXNS 16
|||||
DB 9 DSVCPQGGYIHPOXNS 24

RESULT 5
US-10-125-062-9
; Sequence 9, Application US/10125062
; Publication No. US20020192690A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Xenoport, Inc.
; TITLE OF INVENTION: Epitope-Captured Antibody Display
; FILE REFERENCE: 019282-000710US
; CURRENT APPLICATION NUMBER: US/10/125.062
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/284,305
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:sequence
; OTHER INFORMATION: displayed by fd hTNFR-1 cDNA fragment phage clone
; OTHER INFORMATION: selected for binding to goat anti-hTNFR polyclonal
US-10-125-062-9

Query Match 97.7%; Score 86; DB 9; Length 49;

Best Local Similarity 93.8%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQXNS 16
 |||||
Db 8 DSVCPQGYIHPQXNS 23
 |||||

RESULT 6
US-10-125-062-3
; Sequence 3, Application US/10125062
; Publication No. US20020192690A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Xenoport, Inc.
; TITLE OF INVENTION: Epitope-Captured Antibody Display
; FILE REFERENCE: 019282-000710US
; CURRENT APPLICATION NUMBER: US/10/125,062
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/284,305
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: displayed by T7 htmfr-1 cDNA fragment phage clone
; OTHER INFORMATION: selected for binding to the goat anti-htmfr
; OTHER INFORMATION: polyclonal antibody
US-10-125-062-3

Query Match 97.7%; Score 86; DB 9; Length 69;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQXNS 16
 |||||
Db 11 DSVCPQGYIHPQXNS 26
 |||||

RESULT 7
US-09-882-735-4
; Sequence 4, Application US/09882735
; Publication No. US20030054439A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor "t/pe-I and
; FILE REFERENCE: 02-006
; CURRENT APPLICATION NUMBER: US/09/882,735
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,354
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: stnfr-I
; OTHER INFORMATION: 2.6D/CI05
US-09-882-735-4

Query Match 97.7%; Score 86; DB 9; Length 106;
Best Local Similarity 93.8%; Pred. No. 5.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQXNS 16
 |||||
Db 2 DSVCPQGYIHPQXNS 17
 |||||

RESULT 8
US-09-882-735-8
; Sequence 8, Application US/09882735
; Publication No. US20030054439A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; FILE REFERENCE: 02-006
; CURRENT APPLICATION NUMBER: US/09/882,735
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,354
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: stnfr-I
; OTHER INFORMATION: 2.6D/NI05
US-09-882-735-8

Query Match 97.7%; Score 86; DB 9; Length 106;
Best Local Similarity 93.8%; Pred. No. 5.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQXNS 16
 |||||
Db 2 DSVCPQGYIHPQXNS 17
 |||||

RESULT 9
US-09-882-735-6
; Sequence 6, Application US/09882735
; Publication No. US20030054439A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary

```
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; TITLE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006
; CURRENT APPLICATION NUMBER: US/09/882,735
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,354
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: STNPK-I
; OTHER INFORMATION: 2.6D/C106
US-09-882-735-6

Query Match          97.7%  Score 86:  DB 9:  Length 109;
Best Local Similarity 93.8%  Pred. No. 5.9e-07;
Matches 15:  Conservative 0:  Mismatches 1:  Indels 0:  Gaps 0:

Qy  1  DSVCPQGYIHPQXNS 16
Db  2  DSVCPQGYIHPQXNS 17

RESULT 10
US-09-898-234-4
; Sequence 4, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins, and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-234-4

Query Match          97.7%  Score 86:  DB 9:  Length 161;
Best Local Similarity 93.8%  Pred. No. 8.8e-07;
Matches 15:  Conservative 0:  Mismatches 1:  Indels 0:  Gaps 0:

Qy  1  DSVCPQGYIHPQXNS 16
Db  2  DSVCPQGYIHPQXNS 17

RESULT 11
US-09-899-429A-4
; Sequence 4, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-429A-4

Query Match          97.7%  Score 86:  DB 9:  Length 161;
Best Local Similarity 93.8%  Pred. No. 8.8e-07;
Matches 15:  Conservative 0:  Mismatches 1:  Indels 0:  Gaps 0:

Qy  1  DSVCPQGYIHPQXNS 16
Db  1  DSVCPQGYIHPQXNS 16

RESULT 12
US-09-792-356-4
; Sequence 4, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
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FILE REFERENCE: 98,385-H
CURRENT APPLICATION NUMBER: US/09/899,422
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 4
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-792-356-4

Query Match 97.7%; Score 86; DB 9; Length 161;
Best Local Similarity 93.8%; Pred. No. 8.8e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
Db 1 DSVCPQGYIHPQXNS 16

RESULT 13
US-09-882-735-2

Sequence 2, Application US/09882735
Publication No. US20030054439A1
GENERAL INFORMATION:
APPLICANT: Fisher F., Eric
APPLICANT: Edwards K., Carl
APPLICANT: Kieft L., Gary
TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
TITLE OF INVENTION: Type-II Receptors
FILE REFERENCE: 02-006
CURRENT APPLICATION NUMBER: US/09/882,735
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/214,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US97/12244
PRIOR FILING DATE: 1997-07-09
PRIOR APPLICATION NUMBER: 60/039,792
PRIOR FILING DATE: 1997-03-04
PRIOR APPLICATION NUMBER: 60/039,314
PRIOR FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: 60/037,737
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 60/032,354
PRIOR FILING DATE: 1996-12-06
PRIOR APPLICATION NUMBER: 60/021,443
PRIOR FILING DATE: 1996-07-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 2
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-882-735-2

Query Match 97.7%; Score 86; DB 9; Length 161;
Best Local Similarity 93.8%; Pred. No. 8.8e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
Db 1 DSVCPQGYIHPQXNS 16

RESULT 14
US-09-899-422-4

Sequence 4, Application US/09899422
Patent No. US20020090676A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and TNAS Coding for

FILE REFERENCE: 98,385-H
CURRENT APPLICATION NUMBER: US/09/899,422
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 4
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-899-422-4

Query Match 97.7%; Score 86; DB 10; Length 161;
Best Local Similarity 93.8%; Pred. No. 8.8e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHPQXNS 16
Db 1 DSVCPQGYIHPQXNS 16

RESULT 15
US-09-907-263-2

Sequence 2, Application US/09907263
Patent No. US20020119924A1
GENERAL INFORMATION:
APPLICANT: Sennello, Alison M.
Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/907,263
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/326,394
FILING DATE: 1999-06-04
APPLICATION NUMBER: US 60/036,355
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: US 60/052,023
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zindrick, Thomas K.
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: A-430D
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-907-263-2

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```

Query Match          97.7%; Score 86; DB 10; Length 161;
Best Local Similarity 93.8%; Pred. No. 8.8e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 DSVCPQGGKIHPQXNS 16
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Db 1 DSVCPQGGKIHPQXNS 16

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Job time : 17 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:23:32 ; Search time 16 seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-10-036-434-1

Perfect score: 88
Sequence: 1 DSVCPQGYIHPOXNS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	86	97.7	455	1 GQHUT1	tumor necrosis fac
2	71	80.7	461	1 GQRTT1	tumor necrosis fac
3	70	79.5	454	1 GOMST1	tumor necrosis fac
4	67	76.1	461	2 JCA302	tumor necrosis fac
5	46	52.3	649	2 T46500	hypothetical prote
6	45.5	51.7	843	2 A27131	epidermal growth f
7	45	51.1	198	2 A96811	unknown protein tr
8	45	51.1	1000	2 JE0110	mitotic control pr
9	45	51.1	1043	2 T19734	hypothetical prote
10	45	51.1	3034	2 T14119	seven-pass transme
11	43	48.9	311	2 H70388	seriophosphate sy
12	43	48.9	416	2 S76310	hypothetical prote
13	42	47.7	251	2 S75084	hypothetical prote
14	42	47.7	258	2 H82265	conserved hypothet
15	42	47.7	337	2 F96507	hypothetical prote
16	42	47.7	426	2 T47365	hypothetical prote
17	42	47.7	747	2 I51579	complement factor
18	42	47.7	948	1 A34416	hydroxymethylgluta
19	41	46.6	145	2 F64707	hypothetical prote
20	40	45.5	98	2 D30338	exonuclease DNA-bi
21	40	45.5	108	2 B81890	hypothetical prote
22	40	45.5	276	2 D84021	hypothetical prote
23	40	45.5	395	2 F84160	glutathione-S-trans
24	39	44.3	143	2 S42579	Gln3 protein - fun
25	39	44.3	238	2 F69352	branched-chain ami
26	39	44.3	469	1 I38950	RNA-directed DNA p
27	39	44.3	469	1 I46076	hypothetical prote
28	39	44.3	476	2 T27618	hypothetical prote
29	39	44.3	483	2 A53918	chitinase (EC 3.2.

30	39	44.3	1743	2 T36859	hypothetical prote
31	39	44.3	2297	2 T34918	polyketide synthas
32	38	43.2	72	2 S62621	hydrophobin HFBI -
33	38	43.2	97	2 S62625	hydrophobin HFBI -
34	38	43.2	148	2 B43663	host-inducible pro
35	38	43.2	222	2 AD2105	hypothetical prote
36	38	43.2	390	2 T27256	hypothetical prote
37	38	43.2	506	2 A40679	transcription enha
38	38	43.2	523	2 B40679	transcription enha
39	38	43.2	538	2 G69317	conserved hypothet
40	38	43.2	623	2 A48315	lamin U1 - Africa
41	38	43.2	662	2 S51971	probable membrane
42	38	43.2	677	2 C42125	trophozoite cystel
43	38	43.2	837	2 T00355	hypothetical prote
44	38	43.2	948	2 G83264	hypothetical prote
45	38	43.2	1376	2 S63986	collagen alpha 5 c

ALIGNMENTS

RESULT 1

GQHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A602
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localizatio
A:Reference number: A38208; MUID:92250049; PMID:1315717
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:q339748; PIDN:AAA61201.1
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Genetz, R.; Brockhaus, M.; Tabuchi, H.;
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis facto
A:Reference number: A34899; MUID:90235284; PMID:2158862
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M33480; NID:q339753; PIDN:AAA36753.1; PID:q3397
A:Experimental source: placenta
A:Note: part of this sequence, including the amino end of the mature protein, con
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, C.H.W.; Gatan
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis
A:Reference number: A34900; MUID:90235285; PMID:2158863
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:q339744; PIDN:AAA03210.1; PID:q339745
R:Himmier, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmayer, K.; Lant
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:q339755; PIDN:AAA36754.1; PID:q339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38; 41-53; 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104; 107-128; 162-167; 'X
A:Note: the purified protein, called tumor necrosis factor binding protein, is a
R:Gray, P.W.; Barrett, K.; Chantray, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expressio
A:Reference number: A38281; MUID:91017509; PMID:2170974
A:Accession: A38281
A:Molecule type: mRNA

A:Residues: 1-455 <GB>
A:Cross-references: GB:M37764
A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwarg, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
Ie form of the receptor.
A:Reference number: S12057; MUID:91006021; PMID:1698610
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NOP>
A:Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A:Reference number: J70758; MUID:94085779; PMID:8262379
A:Accession: J70758
A:Molecule type: DNA
A:Residues: 1-133 <KEY>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43,'X',45-53,'X',55-57 <SBC>
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Scubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2151136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: JC2404; MUID:95128033; PMID:7765720
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNPR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/3; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 97.7%; Score 86; DB 1; Length 455;
Best Local Similarity 93.8%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DSVCPQCKYIHPOXNS 16
Db 41 DSVCPQCKYIHPOXNS 56
RESULT 2
GOMST1
tumor necrosis factor receptor 1 precursor - rat
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C:Accession: B36555
R:Himmeler, A.; Maurer-Poggy, I.; Kroenke, M.; Schourich, P.; Pfizenmaier, K.; Lantz,
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor re
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <HIM>
A:Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:30-201/Product: tumor necrosis factor binding protein #status predicted <TUP>
F:84-126/Domain: NGF receptor repeat homology <NG1>
F:127-167/Domain: NGF receptor repeat homology <NG2>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-461/Domain: intracellular #status predicted <INT>
F:54,151,201/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 80.7%; Score 71; DB 1; Length 461;
Best Local Similarity 68.8%; Pred. No. 0.00071;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DSVCPQCKYIHPOXNS 16
Db 41 DNLCPQCKYAHPKNS 56

RESULT 3
GOMST1
tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 10-Jun-1992 #text_change 01-Dec-2000
C:Accession: A38634; B40254; S16677; S19021; S154532; S157826
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Che
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis fac
A:Reference number: A38634; MUID:91187885; PMID:1849278
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA38751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.C.;
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors

A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <GO>
A:Cross-references: GB:M60468; NID:q199825; PIDN:AAA39751.1; PID:q199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissner-Ghis, A.M.; Gray, P.W.; Feldman, J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor type 1
A:Reference number: S16677; MUID:91285014; PMID:1647956
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA1922.1; PID:g53579
R:Rothe, J.G.; Broekhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815; PMID:1657766
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F. Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line
A:Reference number: I54532; MUID:94245292; PMID:8188324
A:Accession: I54532
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: GB:L26349; NID:q430732; PIDN:AAA59361.1; PID:q430733
R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M. Mol. Immunol. 30, 165-176, 1993
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor receptor type 1
A:Reference number: I57826; MUID:93156721; PMID:8381515
A:Accession: I57826
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-393, 'G', 395-454 <RE2>
A:Cross-references: GB:M76656; NID:q202100; PIDN:AAA40465.1; PID:q202102
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
C:Genetics:
A:Gene: TNFR-2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <EXT>
F:30-212/Domain: extracellular #status predicted <NG1>
F:44-82/Domain: NGF receptor repeat homology <NG2>
F:84-126/Domain: NGF receptor repeat homology <NG3>
F:127-167/Domain: NGF receptor repeat homology <NG4>
F:168-204/Domain: NGF receptor repeat homology <NG5>
F:213-235/Domain: transmembrane #status predicted <MEM>
F:236-454/Domain: intracellular #status predicted <INT>
F:34,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.5%; Score 70; DB 1; Length 454;
Best Local Similarity 68.8%; Pred. No. 0.001;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSVCPCKKYTHPOXNS 16
II:IIIIII:II
Db 41 DSLCPCKKYVHSKNS 56

RESULT 4
JC4302
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U. Gene 163, 263-266, 1995

A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: GB:U19994; NID:gl141752; PIDN:AA48499.1; PID:gl141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NGF>
F:211-231/Domain: transmembrane #status predicted <TMM>
F:361-447/Domain: signal transduction #status predicted <SIT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 67; DB 2; Length 461;
Best Local Similarity 68.8%; Pred. No. 0.0032;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSVCPCKKYTHPOXNS 16
II:IIIIII:II
Db 41 ESLCPCKKYSHQNR 56

RESULT 5
T46500
hypothetical protein DKFZp434D098.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46500
R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Cassanhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A:Reference number: 223031
A:Accession: T46500
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-649 <AAA>
A:Cross-references: EMBL:AL137564
A:Experimental source: adult testis; clone DKFZp434D098
C:Genetics:
A:Note: DKFZp434D098.1

Query Match 52.3%; Score 46; DB 2; Length 649;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVCPCKKYTHP 12
II:IIII:II
Db 13 TMCPEGRYGH 23

RESULT 6
A27131
epidermal growth factor receptor - fruit fly (Drosophila melanogaster) (fragment);
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-May-1997
C:Accession: A27131
R:Schejter, E.D.; Segal, D.; Glazer, L.; Shilo, B.Z. Cell 46, 1091-1101, 1986
A:Title: Alternative 5' exons and tissue-specific expression of the Drosophila EGF receptor
A:Reference number: A27131; MUID:87002474; PMID:3093080
A:Accession: A27131
A:Molecule type: mRNA
A:Residues: 1-843 <SCH>
C:Genetics:

A:Gene: FlyBase:Egfr
 A:Cross-references: FlyBase:FBgn0003731
 C:Superfamily: epidermal growth factor receptor; protein kinase homology
 C:Keywords: Atp; growth factor receptor

Query Match 51.7%; Score 45.5; DB 2; Length 843;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Oy 1 DSVCPQG---KYIHPQ 13
 ||||| :||:|
 Db 659 DDKCPDGYFEYVHPQ 674

RESULT 7
 A96811
 unknown protein Tl1111.11 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: A96811
 R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.K.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, K.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96811
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-198 <STO>
 A:Cross-references: GB:AF005173; NID:96587865; PIDN:AAF10551.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: Tl1111.11
 A:Map position: 1

Query Match 51.1%; Score 45; DB 2; Length 198;
 Best Local Similarity 50.0%; Pred. No. 5.5;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 3 VCPOCKYTHPOXNS 16
 ||| :||:|
 Db 170 VCPNCKFHPHDS 183

RESULT 8
 JE0110
 mitotic control protein dis3 homolog - human
 C:Species: Homo sapiens (man)
 C:Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 02-Nov-2001
 C:Accession: JE0110; T12542
 R:Shiomi, T.; Fukushima, K.; Suzuki, N.; Nakashima, N.; Noguchi, E.; Nishimoto, T.
 J. Biochem. 123, 883-890, 1998
 A:Title: Human Dis3, which binds to either GTP- or GDP-Ran, complements Saccharomyces ce
 A:Reference number: JE0110; MUID:98230695; PMID:9562621
 A:Accession: JE0110
 A:Molecule type: mRNA
 A:Residues: 1-1000 <SH>
 R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Cassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: T12542
 A:Accession: T12542
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 369-593, K', 595-1000 <WAM>
 A:Cross-references: EMBL:AL080158
 A:Experimental source: adult testis; clone DKF2p434L194
 C:Comment: This protein enhances a temperature-sensitive mutant RCC1-stimulated nucleoti
 C:Genetics:

A:Note: DKF2p434L194.1
 C:Superfamily: mitotic control protein dis3

Query Match 51.1%; Score 45; DB 2; Length 1000;
 Best Local Similarity 57.1%; Pred. No. 26;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 SVCPOGKYIHPQXN 15
 ||||| :||:|
 Db 58 SVCPOPHYLLPDTN 71

RESULT 9
 T19734
 hypothetical protein C34F6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T19734
 R:White, S.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19171
 A:Accession: T19734
 A:Status: preliminary; translated from GB/EMBL/DD8J
 A:Molecule type: DNA
 A:Residues: 1-1043 <WIL>
 A:Cross-references: EMBL:Z81479; PIDN:CAR03944.1; GSPDB:GN00028; CESP:C34F6.1
 A:Experimental source: clone C34F6
 C:Genetics:
 A:Gene: CESP:C34F6.1
 A:Map position: X
 A:Introns: 17/3; 62/1; 129/3; 181/1; 292/1; 348/1; 404/1; 665/1; 769/1; 876/1; 977/

Query Match 51.1%; Score 45; DB 2; Length 1043;
 Best Local Similarity 63.6%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DSVCPQGYIHP 11
 ||||| :||:|
 Db 322 DSMCPNGYYCH 332

RESULT 10
 T14119
 seven-pass transmembrane receptor protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14119
 R:Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
 submitted to the EMBL Data Library, October 1997
 A:Description: The Ce1sr family of novel evolutionarily conserved seven-pass transm
 A:Reference number: Z17881
 A:Accession: T14119
 A:Status: preliminary; translated from GB/EMBL/DD8J
 A:Molecule type: mRNA
 A:Residues: 1-3034 <HAD>
 A:Cross-references: EMBL:AF031572; NID:93800735; PID:93800736; PIDN:ACC68836.1
 C:Genetics:
 A:Gene: Ce1sr1
 A:Map position: 15

C:Keywords: transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-3034/product: seven-pass transmembrane receptor protein #status predicted <MAT

Query Match 51.1%; Score 45; DB 2; Length 3034;
 Best Local Similarity 70.0%; Pred. No. 74;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 VCPOCKYIHP 12
 ||| :||:|
 Db 1444 VCPGGEYHP 1453

RESULT 11

H70388
 selenophosphate synthase - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
 C:Accession: H70388
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: H70388
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-311 <AOE>
 A:Cross-references: GB:AE000719; NID:q2983517; PIDN:AAC07095.1; PID:q2983519; GB:AE00065
 A:Experimental source: strain VF5
 C:Genetics: self
 C:Superfamily: conserved hypothetical protein M70640

Query Match 48.9%; Score 43; DB 2; Length 311;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VCPQGYI 10
 :||:||||
 Db 123 ICPEGYI 130

RESULT 12
 S76310
 hypothetical protein - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 s.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76310
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-416 <KAN>
 A:Cross-references: EMBL:D64000; GB:AB001339; NID:q1001484; PIDN:BAAL0162.1; PID:q100153
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 48.9%; Score 43; DB 2; Length 416;
 Best Local Similarity 77.8%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PCKGYIHPQ 13
 :|||:||||
 Db 274 PCKGYIHPQ 282

RESULT 13
 S75084
 hypothetical protein sll0249 - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 s.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S75084
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-251 <KAN>
 A:Cross-references: EMBL:P90910; GB:AB001339; NID:q1652956; PIDN:BAAL7946.1; PID:
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 47.7%; Score 42; DB 2; Length 251;
 Best Local Similarity 46.7%; Pred. No. 21;
 Matches 7; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

QY 3 VCPQGYI----HPQ 13
 :||:||||
 Db 211 LCPEGKYVFFEHPE 225

RESULT 14
 H82265
 conserved hypothetical protein VC0904 [imported] - Vibrio cholerae (strain N16961)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: H82265
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson
 chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sel
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: H82265
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <HEI>
 A:Cross-references: GB:AE004174; GB:AE003852; NID:q9655355; PIDN:AAF94066.1; CSPE
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0904
 A:Map position: 1

Query Match 47.7%; Score 42; DB 2; Length 258;
 Best Local Similarity 40.0%; Pred. No. 22;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 SVCPOGKYIHPQXNS 16
 :|||: :||: :||
 Db 54 AVCPEKESLHPKPHS 68

RESULT 15
 F96507
 hypothetical protein T12C22.12 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: F96507
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dew
 angen, N.F.; Hughes, B.; Huizlar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luo, J.S.; Maity, R.; Ma
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96507
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-337 <STO>
 A:Cross-references: GB:AE005173; NID:q8655995; PIDN:AAF78268.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T12C22.12
 A:Map position: 1

Query Match 47.7%; Score 42; DB 2; Length 337;
 Best Local Similarity 63.6%; Pred. No. 28;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 3 VCPQGYIHPQ 13
 || :|| ||:
 Db 5 VCEKGCIHPR 15

Search completed: May 21, 2003, 18:28:05
 Job time : 19 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:09:52 ; Search time 11 seconds
(without alignments)
60,329 Million cell updates/sec

Title: US-10-036-434-1

Perfect score: 88

Sequence: 1 DSVCPQCKYIHPOXNS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	97.7	455	1 TRIA_HUMAN	P19438 homo sapien
2	71	80.7	461	1 TRIA_RAT	P22934 rattus norv
3	70	79.5	454	1 TRIA_MOUSE	P25118 mus musculu
4	67	76.1	461	1 TRIA_PIG	P05055 sus scrofa
5	61	69.3	471	1 TRIA_BOVIN	O19131 bos taurus
6	45.5	51.7	1426	1 EGFR_DROME	P04412 drosophila
7	45	51.1	928	1 RK44_HUMAN	O9v211 homo sapien
8	45	51.1	3034	1 CLR1_MOUSE	O35161 mus musculu
9	43	48.9	336	1 SELD_AQUAE	O67139 aquifex aeo
10	42	47.7	251	1 Y249_SYNY3	P73883 synchocyst
11	42	47.7	948	1 HMDL_SCHMA	P16237 schistosoma
12	40	45.5	98	1 CMGC_BACSIU	P25955 bacillus su
13	39.5	44.9	787	1 ST5B_PIG	O9tuz0 sus scrofa
14	39.5	44.9	799	1 ST5A_PIG	O9tuz1 sus scrofa
15	39	44.3	143	1 Q103_TRIHA	P52755 trichoderma
16	39	44.3	469	1 DPD2_BOVIN	P49004 bos taurus
17	39	44.3	469	1 DPD2_HUMAN	P49005 homo sapien
18	39	44.3	469	1 DPD2_MOUSE	O35654 mus musculu
19	39	44.3	514	1 EDAR_ORYLA	O90vY2 oryzias lat
20	38	43.2	97	1 HYP1_TRIPE	P52754 trichoderma
21	38	43.2	148	1 NOIJ_RHIFR	P12780 rhizobium f
22	38	43.2	448	1 K1M2_HUMAN	Q14532 homo sapien
23	38	43.2	449	1 PLSV_ADEM1	P12539 mouse adeno
24	38	43.2	463	1 PLVB_CARTI	O42713 carthamus t
25	38	43.2	521	1 CP11_LIMLI	O42430 limanda lim
26	38	43.2	528	1 GD_DROME	O62589 drosophila
27	38	43.2	623	1 LAM2_XENLA	P21910 xenopus lae
28	38	43.2	630	1 AT54_RAT	O9esp7 rattus norv
29	38	43.2	662	1 YAE8_YEAST	P39722 saccharomyc
30	38	43.2	837	1 AT54_HUMAN	O75173 homo sapien
31	38	43.2	1586	1 AROL_EMENT	P07547 e pentafunc
32	37.5	42.6	351	1 NOV_CHICK	P28686 gallus gall
33	37.5	42.6	353	1 NOV_COTJA	P42642 coturnix co

ALIGNMENTS

RESULT 1

ID	TRIA_HUMAN	STANDARD:	PRT:	455 AA.
AC	P19438:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor			
DE	binding protein 1 (TBPI)]			
GN	TNFRSF1A OR TNFR1 OR TNFR			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	N:001_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,			
RA	Gatanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;			
RT	"Molecular cloning and expression of a receptor for human tumor			
RT	necrosis factor."			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Bröckhaus M.,			
RA	Tabuchi H., Lesslauer W.;			
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis			
RT	factor receptor."			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RX	MEDLINE=91006021; PubMed=1698610;			
RA	Noplar Y., Kemper O., Brakebusch C., Engelmann H., Zhang R.,			
RA	Aderka U., Holtmann H., Wallach D.;			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA			
RT	for the type I TNF-R, cloned using amino acid sequence data of its			
RT	soluble form, encodes both the cell surface and a soluble form of the			
RT	receptor."			
KL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,			
RA	Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;			
RT	"Molecular cloning and expression of human and rat tumor necrosis			
RT	factor receptor chain (p60) and its soluble derivative, tumor			
RT	necrosis factor-binding protein."			
KL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			

P20925 proteus vul
O8wxk2 homo sapien
P41935 cecorhabdi
O92095 opsanus lau
O9vh64 platichthys
O92100 pleuronacte
P39358 escherichia
O91009 gallus gall
O9gyp2 rattus norv
O9r0m0 mus musculu
O9hcu4 homo sapien
O9nyq6 homo sapien

34 37 42.0 157 1 YPRA_PROVU
35 37 42.0 302 1 AS14_HUMAN
36 37 42.0 344 1 HM10_CAEBL
37 37 42.0 521 1 CP11_OPSTA
38 37 42.0 521 1 CP11_PLAFE
39 37 42.0 521 1 CP11_PLEPL
40 37 42.0 655 1 YJIG_ECOLT
41 37 42.0 778 1 TRKA_CHICK
42 37 42.0 2144 1 CLK2_RAT
43 37 42.0 2920 1 CLK2_MOUSE
44 37 42.0 2423 1 CLK2_HUMAN
45 37 42.0 3014 1 CLK1_HUMAN

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
 RL expression of recombinant soluble TNF-binding protein.";
 RN Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92250049; PubMed-1315717;
 RA Fuchs P., Strehl S., Dvorzak M., Himmler A., Ambros P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 RL localization to chromosome 12p13.";
 RN Genomics 13:219-224(1992).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93258809; PubMed-8387891;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RL urine. Evidence for immunological cross-reactivity with cell surface
 RN tumor necrosis factor receptors.";
 RP J. Biol. Chem. 265:1531-1536(1990).
 RX MEDLINE-93258809; PubMed-8387891;
 RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 RL beta complex: Implications for TNF receptor activation.";
 RN Cell 73:431-445(1993).
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE-97094982; PubMed-8939750;
 RA Naimsmith J.H., Devine T.O., Khono H., Sprang S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis
 RL factor receptor.";
 RN Structure 4:1251-1262(1996).
 RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
 RX MEDLINE-99213501; PubMed-10199409;
 RA McDermott M.F., Aksentjevich I., Galon J., McDermott E.M.,
 RL Ogunkolade B.W., Centola J., Mansfield E., Gadina M., Karenko L.,
 RA Petterson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
 RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
 RA Schlimmer R., Kumarajew T.R., Cooper S.M., Vella J.P., Amos C.I.,
 RA Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
 RA Hitman G.A., O'Shea J., Kastner D.L.;
 RT "germline mutations in the extracellular domains of the 55 kDa TNF
 RL receptor, TNFR1, define a family of dominantly inherited
 RL autoinflammatory syndromes.";
 CC Cell 97:133-144(1999).
 CC -1- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric
 CC TNFSP1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis. Contributes to
 CC the induction of noncytotoxic TNF effects including anti-viral
 CC state and activation of the acid sphingomyelinase.
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -1- PTM: The soluble form is produced from the membrane form by

CC proteolytic processing.
 CC -1- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
 CC familial hibernian fever (FHF), a disease characterized by
 CC recurrent fever, abdominal pain, localized tender skin lesions and
 CC myalgia.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- DATABASE: NAME=PROW; NORT=CD guide CD120a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
 CC -----
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 CC -----
 CC EMBL: X55313; CAA39021.1; -
 CC EMBL: M31294; AAA03210.1; -
 CC EMBL: M58286; AAA36753.1; -
 CC EMBL: M63121; AAA36754.1; -
 CC EMBL: M75866; AAA61201.1; -
 CC EMBL: M75864; AAA61201.1; JOINED.
 CC EMBL: M75865; AAA61201.1; JOINED.
 CC EMBL: M60275; AAA36756.1; -
 CC EMBL: A21522; CAA01558.1; -
 CC EMBL: BC010140; AAH10140.1; -
 CC PIR: A34899; G0HU11.
 CC PIR: A35010; A35010.
 CC PIR: S12057; S12057.
 CC PIR: A38208; A38208.
 CC PDB: 1TNK; 31-JUL-94.
 CC PDB: 1NCF; 07-DEC-95.
 CC PDB: 1EXT; 11-JAN-97.
 CC Genew: H0NC11916; TNFRSF1A.
 CC MIM: 191190; -
 CC MIM: 142680; -
 CC InterPro: IPR000488; Death.
 CC InterPro: IPR001368; TNFR_c6.
 CC Pfam: PF00020; TNFR_c6; 4.
 CC Pfam: PF00531; death; 1.
 CC ProDom: PD000771; TNFR_c6; 1.
 CC SMART: SM00005; DEATH; 1.
 CC SMART: SM00208; TNFR; 4.
 CC PROSITE: PS00652; TNFR_NGFR_1; 3.
 CC PROSITE: PS50050; TNFR_NGFR_2; 3.
 CC PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Disease mutation; Polymorphism; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 1A, MEMBRANE FORM.
 FT CHAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 234 POTENTIAL.
 FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 356 441 DEATH.
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179

Query Match 97.7%; Score 86; DB 1; Length 455;
Best Local Similarity 93.8%; Pred. No. 8.5e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSVCPQGRYTHPOXNS 16
IIIIIIIIIIIIIIII
Db 41 DSVCPQGRYTHPOXNS 56

RESULT 2
TRIA_RAT STANDARD; PRT; 461 AA.
AC P22934; Q91V30; Q91Y93;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Hummer A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC STRAIN-Variou;
RA Furuya T., Salstrom J.L., Bina J., Hashimoto A., Robbins D.E.,
RA Wilder R.L., Remmers E.F.;
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT among autoimmune susceptible and resistant inbred rat strains";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for TNFSE2/TNF-alpha and hemotrimer-2
CC TNFSE1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (unstable-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNF1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNF1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL: M63122; AAA42256.1; -
DR EMBL: AF329976; AAK53562.1; -
DR EMBL: AF329977; AAK53563.1; -
DR EMBL: AF329981; AAK53567.1; -
DR EMBL: AF329978; AAK53564.1; -
DR EMBL: AF329979; AAK53565.1; -

EMBL: AF329980; AAK53566.1; -
DR PIR: B36555; R36555.
DR HSP: P19438; INCF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 4.
DR Pfam: PF00531; death; 1.
DR PRODOM: PD000771; TNFR_C6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00050; TNFR_NGFR_2; 3.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT CHAIN 1 21
FT SIGNAL 22 461
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 344 354
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 195
FT DISULFID 185 191
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
FT VARIANT 230 230
FT VARIANT 295 295
FT SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;

Query Match 80.7%; Score 71; DB 1; Length 461;
Best Local Similarity 68.8%; Pred. No. 0.00025;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DSVCPQGRYTHPOXNS 16
IIIIIIIIIIIIIIII
Db 41 DSVCPQGRYTHPOXNS 56

RESULT 3
TRIA_MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A.V., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is shared
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brennan C.J.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.,
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91285014; PubMed=1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.,
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Spleen;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.,
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94245292; PubMed=9188324;
 RA Bebo B.F., Linthicum D.S.,
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line.";
 RL Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93156721; PubMed=8381516;
 RA Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.,
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175(1993).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric
 CC TNFSP1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (by similarity).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M60468; AAA39751.1; -
 DR EMBL: M59377; AAA04064.1; -
 DR EMBL: X59238; CAA41922.1; -
 DR EMBL: X57796; CAA40936.1; -
 DR EMBL: L26349; AAA59361.1; -
 DR EMBL: M76656; AAA04065.1; -
 DR EMBL: M88057; AAA04065.1; JOINED.
 DR EMBL: M76655; AAA04065.1; JOINED.
 DR EMBL: BC004599; AAA04599.1; -
 DR PIR: A38634; GOMST1.
 DR PIR: S16677; S16677.
 DR PIR: S19021; S19021.
 DR HSSP: P19438; 1EXT.
 DR MGD: MGI:1314884; Tnftrsf1a.
 DR InterPro: IPR000488; Death.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR Pfam: PF00531; death; 1.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00050; TNFR_NGFR_2; 3.
 DR PROSITE: PS00017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR
 FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 213 235 POTENTIAL.
 FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 339 349 N-SHASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 356 441 DEATH.
 FT DISULFID 44 58. BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 185 191 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 79.5%; Score 70; DR 1; Length 454;
 Best Local Similarity 68.8%; Pred. No. 0.00035;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 DSVCPCKGYTHPOXNS 16
 II:IIIIII:II:II
 Db 41 DSLCPCKGYVHSKNS 56

RESULT 4
 ID TRIA_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (P55).


```

DR PRODOM: PD000771; TNFR_C6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR.1; 3.
DR PROSITE: PS00050; TNFR_NGFR.2; 3.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 22 210 SUPERFAMILY MEMBER 1A.
FT TRANSMEM 211 233 EXTRACELLULAR (POTENTIAL).
FT REPEAT 234 471 POTENTIAL.
FT REPEAT 43 82 CYTOPLASMIC (POTENTIAL).
FT REPEAT 83 125 TNFR-CYS 1.
FT REPEAT 126 166 TNFR-CYS 2.
FT REPEAT 167 195 TNFR-CYS 3.
FT REPEAT 196 233 TNFR-CYS 4.
FT DOMAIN 340 360 N-SHASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 372 457 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 194 BY SIMILARITY.
FT DISULFID 185 190 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 471 AA; 51367 MW; 5243EF514DFE81C4; Cys64;

Query Match 69.3%; Score 61; DB 1; Length 471;
Best Local Similarity 62.5%; Pred. No. 0.011;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSVCPGKGYTHPOXNS 16
DB 41 ESPCPGKYNHPQNST 56

RESULT 6
EGFR_DROME STANDARD: PRT; 1426 AA.
AC P04412; O61601; Q9W2G0; P81868;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)
DE (Gurken receptor) (Torpedo protein) (Drosophila relative of FRBB).
GN EGFR OR TOP OR C-ERBB OR DER OR CG10079.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II).
MEDLINE=94350209; PubMed=8070664;
Clifford R., Schupbach T.;
"molecular analysis of the Drosophila EGF receptor homolog reveals
that several genetically defined classes of alleles cluster in
subdomains of the receptor protein.";
Genetics 137:531-550(1994).
[2]
REVIEWS.
RP Clifford R., Schupbach T.;
KL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[3]

SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=85124611; PubMed=2982499;
Livneh E., Glazer L., Segal D., Schlessinger J., Shilo B.-2.;
"The Drosophila EGF receptor gene homolog: conservation of both
hormone binding and kinase domains.";
Cell 40:599-607(1985).
[4]
SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING.
STRAIN=Oregon-K; Tissue=embryo;
MEDLINE=87002474; PubMed=3093080;
Schejter E.D., Segal D., Glazer L., Shilo B.-2.;
"Alternative 5' exons and tissue-specific expression of the
Drosophila EGF receptor homolog transcripts.";
Cell 46:1091-1101(1986).
[5]
SEQUENCE FROM N.A. (ISOFORM TYPE I), TISSUE SPECIFICITY, AND MUTATION
ANALYSIS.
MEDLINE=99102120; PubMed=9882502;
Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
Dev. Biol. 205:129-144(1999).
[6]
SEQUENCE FROM N.A. (ISOFORM TYPE I).
STRAIN=Berkley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
George R.A., Lewis S.E., Richards J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
Cherry K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.R., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Dorbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Purli V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venier E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
[7]
SEQUENCE OF 959-1078 FROM N.A.
STRAIN=Daekwanryeong;
MEDLINE=85137938; PubMed=2983232;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal
growth factor receptor";
Nature 314:178-180(1985).
[8]

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RP SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION ANALYSIS.

RX MEDLINE=92038942; PubMed=1936959;

RA Raz E., Schejter E.D., Shilo B.Z.;

RT "Interallelic complementation among DER/fhb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";

RL Genetics 129:191-201(1991).

RN [9]

RP REVIEW.

RX MEDLINE=97248481; PubMed=9094709;

RA Perrimon N., Perkins L.A.;

RT "There must be 50 ways to rule the signal: the case of the Drosophila EGF receptor.";

RL Cell 89:13-16(1997).

CC -1- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND AKGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS, CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE OOCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEKOSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATE SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF CUTICLE.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine + ADP + protein tyrosine phosphate.

CC -1- SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX AND THORACIC AND ABDOMINAL GLANDS.

CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

CC -----

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CC -----

DR EMBL; AF052754; AAC08536.1; -

DR EMBL; AF052753; AAC08536.1; JOINED.

DR EMBL; AF052754; AAC08535.1; -

DR EMBL; AF052752; AAC08535.1; JOINED.

DR EMBL; K03054; AA51462.1; -

DR EMBL; K03417; AA51460.1; -

DR EMBL; K03416; AA50965.1; -

DR EMBL; K03418; AA51461.1; -

DR EMBL; AF109077; AAD26134.1; -

DR EMBL; AF109078; AAD26132.1; -

DR EMBL; AF109082; AAD26132.1; JOINED.

DR EMBL; AF109078; AAD26133.1; -

DR EMBL; AF109084; AAD26133.1; JOINED.

DR EMBL; AF109079; AAD26130.1; -

DR EMBL; AF109081; AAD26130.1; JOINED.

DR EMBL; AF109079; AAD26131.1; -

DR EMBL; AF109083; AAD26131.1; JOINED.

DR EMBL; AF109080; AAD26135.1; -

DR EMBL; AE003454; AAF46732.1; -

DR EMBL; X02293; CAA26157.1; -

DR EMBL; X78920; CAA55523.1; -

DR EMBL; X78919; CAA55521.1; -

DR EMBL; X78918; CAA55522.1; -

DR PIR; A00640; GOFPE.

DR HSSP; P11362; IFGK.

DR FlyBase: FBgn0003731; Egfr.

DR InterPro: IPR000494; EGFR_L_domain.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR002174; Furin-like.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam: PF00069; pkinase; 1.

DR Pfam: PF00757; Furin-like; 1.

DR Pfam: PF01030; Recep_L_domain; 2.

DR PRINTS: PR0109; TYRKINASE.

DR ProDom: PD000001; Euk_pkinase; 1.

DR SMART: SM00261; FU; 7.

DR SMART: SM00219; TyrKc; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

CC KW Transmembrane: Glycoprotein; Receptor; Phosphorylation; Transferase; Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing; Developmental protein.

CC KW Developmental protein.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 1426 EPIDERMAL GROWTH FACTOR RECEPTOR.

FT DOMAIN 31 868 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 869 889 POTENTIAL.

FT DOMAIN 890 1426 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 938 1198 PROTEIN KINASE.

FT NP_BIND 944 952 ATP (BY SIMILARITY).

FT BINDING 971 971 ATP (BY SIMILARITY).

FT ACT_SITE 1063 1063 BY SIMILARITY.

FT MOD_RES 902 902 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

Query Match 51.7%; Score 45.5; DB 1; Length 1426;

Best Local Similarity 50.0%; Pred. No. 11;

Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

OY 1 DSVCPQC---KYIHPQ 13

DB 708 DDKCPDGYFWYVWIPQ 723

RESULT 7

RR44_HUMAN STANDARD; PRT; 928 AA.

ID RR44_HUMAN

AC Q9Y2L1: O9UC36; O8MW12;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA processing protein 44) (DIS3 protein homology).

DE DIS3 OR RRP44 OR KIAA1008.

GN Homo sapiens (Human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

KN [1]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RX MEDLINE=98210695; PubMed=9562621;

RA Shiomi T., Fukushima K., Suzuki N., Nakashima N., Noguchi E., Nishimoto T.;

RT "Human dis3p, which binds to either GTP- or GDP-Ran, complements Saccharomyces cerevisiae dis3.";

KL J. Biochem. 123:883-890(1998).

RN [2]

RP ERRATUM.

RA Shiomi T., Fukushima K., Suzuki N., Nakashima N., Noguchi E., Nishimoto T.;

KL J. Biochem. 124:250-250(1998).

KN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=99246063; PubMed=10231032;

RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code

DR Pfam: PF00028; cadherin; 9.
 DR Pfam: PF00008; EGF; 6.
 DR Pfam: PF01825; GPs; 1.
 DR Pfam: PF02793; HRM; 1.
 DR Pfam: PF00053; laminin_EGF; 1.
 DR Pfam: PF00054; laminin_G; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR PRINTS: PR00011; EGFLAMININ.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR SMART: SM00112; CA; 9.
 DR SMART: SM00180; EGF_Lam; 1.
 DR SMART: SM00401; EGF_Like; 6.
 DR SMART: SM00303; GPs; 1.
 DR SMART: SM00008; HORMR; 1.
 DR SMART: SM00282; LamG; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 2.
 DR PROSITE: PS00232; CADHERIN_1; 7.
 DR PROSITE: PS00268; CADHERIN_2; 9.
 DR PROSITE: PS00022; EGF_1; 6.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS00221; GPs; 1.
 DR PROSITE: PS00649; G_PROTEIN_RECEPTOR_F2_1; FALSE_NEG.
 DR PROSITE: PS00650; G_PROTEIN_RECEPTOR_F2_2; FALSE_NEG.
 DR PROSITE: PS00227; G_PROTEIN_RECEPTOR_F2_3; 1.
 DR PROSITE: PS00261; G_PROTEIN_RECEPTOR_F2_4; 1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 1.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 2.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
 KW Developmental protein; Signal; Hydroxylation; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 3034
 FT FT
 FT DOMAIN 21 2484
 FT TRANSMEM 2485 2505
 FT DOMAIN 2506 2516
 FT TRANSMEM 2517 2537
 FT DOMAIN 2538 2542
 FT TRANSMEM 2543 2563
 FT DOMAIN 2564 2587
 FT TRANSMEM 2588 2608
 FT DOMAIN 2609 2625
 FT TRANSMEM 2626 2646
 FT DOMAIN 2647 2691
 FT TRANSMEM 2691 2699
 FT DOMAIN 2692 2694
 FT TRANSMEM 2695 2715
 FT DOMAIN 2716 3034
 FT DOMAIN 261 368
 FT DOMAIN 369 474
 FT DOMAIN 475 580
 FT DOMAIN 581 702
 FT DOMAIN 703 804
 FT DOMAIN 805 907
 FT DOMAIN 908 1014
 FT DOMAIN 1015 1116
 FT DOMAIN 1121 1239
 FT DOMAIN 1318 1376
 FT DOMAIN 1378 1414
 FT DOMAIN 1418 1456
 FT DOMAIN 1457 1661
 FT DOMAIN 1664 1700
 FT DOMAIN 1704 1887
 FT DOMAIN 1887 1922
 FT DOMAIN 1923 1961
 FT DOMAIN 1962 1994
 FT DOMAIN 1996 2031
 FT DOMAIN 2037 2070
 FT DOMAIN 2423 2475
 FT DOMAIN 2674 2678
 FT DOMAIN 1322 1333
 FT DISULFID 1327 1364
 FT DISULFID 1366 1375

Pfam: PF00028; cadherin; 9.
 Pfam: PF00008; EGF; 6.
 Pfam: PF01825; GPs; 1.
 Pfam: PF02793; HRM; 1.
 Pfam: PF00053; laminin_EGF; 1.
 Pfam: PF00054; laminin_G; 1.
 PRINTS: PR00205; CADHERIN.
 PRINTS: PR00011; EGFLAMININ.
 PRINTS: PR00249; GPCRSECRETIN.
 SMART: SM00112; CA; 9.
 SMART: SM00180; EGF_Lam; 1.
 SMART: SM00401; EGF_Like; 6.
 SMART: SM00303; GPs; 1.
 SMART: SM00008; HORMR; 1.
 SMART: SM00282; LamG; 2.
 PROSITE: PS00010; ASX_HYDROXYL; 2.
 PROSITE: PS00232; CADHERIN_1; 7.
 PROSITE: PS00268; CADHERIN_2; 9.
 PROSITE: PS00022; EGF_1; 6.
 PROSITE: PS01186; EGF_2; 2.
 PROSITE: PS00221; GPs; 1.
 PROSITE: PS00649; G_PROTEIN_RECEPTOR_F2_1; FALSE_NEG.
 PROSITE: PS00650; G_PROTEIN_RECEPTOR_F2_2; FALSE_NEG.
 PROSITE: PS00227; G_PROTEIN_RECEPTOR_F2_3; 1.
 PROSITE: PS00261; G_PROTEIN_RECEPTOR_F2_4; 1.
 PROSITE: PS01248; LAMININ_TYPE_EGF; 1.
 PROSITE: PS00025; LAM_G_DOMAIN; 2.
 G-protein coupled receptor; Transmembrane; Glycoprotein;
 EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
 Developmental protein; Signal; Hydroxylation; Signal.
 SIGNAL 1 29
 CHAIN 30 3034
 FT
 FT
 FT DOMAIN 21 2484
 FT TRANSMEM 2485 2505
 FT DOMAIN 2506 2516
 FT TRANSMEM 2517 2537
 FT DOMAIN 2538 2542
 FT TRANSMEM 2543 2563
 FT DOMAIN 2564 2587
 FT TRANSMEM 2588 2608
 FT DOMAIN 2609 2625
 FT TRANSMEM 2626 2646
 FT DOMAIN 2647 2691
 FT TRANSMEM 2691 2699
 FT DOMAIN 2692 2694
 FT TRANSMEM 2695 2715
 FT DOMAIN 2716 3034
 FT DOMAIN 261 368
 FT DOMAIN 369 474
 FT DOMAIN 475 580
 FT DOMAIN 581 702
 FT DOMAIN 703 804
 FT DOMAIN 805 907
 FT DOMAIN 908 1014
 FT DOMAIN 1015 1116
 FT DOMAIN 1121 1239
 FT DOMAIN 1318 1376
 FT DOMAIN 1378 1414
 FT DOMAIN 1418 1456
 FT DOMAIN 1457 1661
 FT DOMAIN 1664 1700
 FT DOMAIN 1704 1887
 FT DOMAIN 1887 1922
 FT DOMAIN 1923 1961
 FT DOMAIN 1962 1994
 FT DOMAIN 1996 2031
 FT DOMAIN 2037 2070
 FT DOMAIN 2423 2475
 FT DOMAIN 2674 2678
 FT DOMAIN 1322 1333
 FT DISULFID 1327 1364
 FT DISULFID 1366 1375

Query Match 51.1%; Score 45; DB 1; Length 3034;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VCPQGYIHP 12
 III I I I I
 DU 1444 VCPPEYHP 1453
 ID SELD_AQUAF STANDARD; PRT; 336 AA.
 AC 067139;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Selenide water dikinase (EC 2.7.9.3) (Selenophosphate synthetase)
 DE (Selenide donor protein).
 GN SELD OR AQ_1030.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex.
 QX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=VF5;
 RX MEDLINE=9819666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.C., Leroy A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Auay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson K.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 acolicus.";
 RL Nature 392:353-358(1998).
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RA Baloch A.;
 RL Unpublished observations (JUL-1999).
 CC -!- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND ATP
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + selenide + H(2)O -> AMP + selenophosphate
 CC + phosphate.
 CC -!- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
 CC CLASS 1 SUBFAMILY.
 CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A UGA STOP CODON HAD TO
 CC BE SKIPPED IN POSITION 13 TO PRODUCE THIS ORF. WE (REF.2) BELIEVE
 CC THAT THIS RESIDUES IS MOST PROBABLY AN ACTIVE-SITE SELENOCYSTEINE.
 CC -----
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 CC -----
 CC EMBL: A600719; AAC07095.1; ALT_FRAME.
 DR InterPro: IPR000728; AIRS-related.
 DR InterPro: IPR004536; Seld.
 DR Pfam: PF00586; AIRS: 1.
 DR Pfam: PF02769; AIRS-C: 1.
 DR TIGRfams: TIGR00476; Seld: 1.
 DR Transferrase: Selenum; Magnesium; ATP-binding; Selenocysteine;
 KW Complete proteome.
 FT ACT_SITE 13 13 POTENTIAL.
 FT SE_CYS 13 13 POTENTIAL.
 FT SITE 16 16 IMPORTANT FOR CATALYTIC ACTIVITY (BY
 FT SIMILARITY).
 FT NP_BIND 222 228 ATP (POTENTIAL).
 FT SEQUENCE 336 AA; 36809 MW; D2AA183BC378529D CRC64;
 Query Match 48.9%; Score 43; DB 1; Length 336;
 Best Local Similarity 75.0%; Pred. No. 7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 VCPQGYI 10
 DB 148 ICPEGYI 155
 :||:||||
 RESULT 10
 Y249_SYNY3 STANDARD; PRT; 251 AA.
 AC P73883;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein sl10249.
 GN SLL0249.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- SIMILARITY: TO ANABAENA PCC 7120 ALR2406.
 CC -----
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 CC -----
 CC EMBL: D90910; BAA17946.1;
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 251 AA; 28880 MW; A3FD1ACE6C3C8D4E CRC64;
 Query Match 47.7%; Score 42; DB 1; Length 251;
 Best Local Similarity 46.7%; Pred. No. 7.7;
 Matches 7; Conservative 3; Mismatches 1; Indels 4; Gaps 1;
 QY 3 VCPQGYI-----HPQ 13
 DB 211 LCPEGYKFFQFHEPE 225
 :||:||||
 RESULT 11
 HMDH_SCHMA STANDARD; PRT; 948 AA.
 ID AC P16237;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA
 DE reductase).
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90046767; PubMed=2813388;
 RA Rajkovic A., Simonsen J.N., Davis R.E., Rottman F.M.;
 RT "Molecular cloning and sequence analysis of
 RT 3-hydroxy-3-methylglutaryl-coenzyme A reductase from the human
 RT parasite Schistosoma mansoni.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8217-8221(1989).
 RN [2]
 RP SEQUENCE OF 1-236 FROM N.A.
 RC STRAIN=Puerto Rican;
 RX MEDLINE=95394947; PubMed=7665603;
 RA Davis R.E., Hardwick C., Tavernier P., Hodgson S., Singh H.;
 RT "RNA trans-splicing in flatworms. Analysis of trans-spliced mRNAs and
 RT genes in the human parasite, Schistosoma mansoni.";
 RL J. Biol. Chem. 270:21813-21819(1995).
 CC -!- FUNCTION: THIS TRANSMEMBRANE GLYCOPROTEIN IS INVOLVED IN THE
 CC CONTROL OF CHOLESTEROL AND NONSTEROID ISOPRENOID COMPOUNDS
 CC BIOSYNTHESIS. IT IS THE RATE-LIMITING ENZYME OF STEROL
 CC BIOSYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: (R)-mevalonate + CoA + 2 NADP(+) -> (S)-3-
 CC hydroxy-3-methylglutaryl-CoA + 2 NADPH.
 CC -!- PATHWAY: Cholesterol biosynthesis.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
 CC RETICULUM AND PEROXISOMES.
 CC -!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.
 CC -----
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EMBL: M27294; AAA29896.1; -.
EMBL: U33178; AAC46885.1; -.
PIR: A34416; A34416..
InterPro: IPR002202; HMG-CoA_red.
InterPro: IPR004554; HMG-CoA_R_NADP.
Pfam: PF00368; HMG-CoA_red.1.
PRINTS: PR00071; HMGCOORDTASE.
TIGRfam: TIGR00533; HMG-CoA_R_NADP.1.
PROSITE: PS00066; HMG-CoA_REDUCTASE.1; 1.
PROSITE: PS00318; HMG-CoA_REDUCTASE.2; 1.
PROSITE: PS01192; HMG-CoA_REDUCTASE.3; 1.
PROSITE: PS50065; HMG-CoA_REDUCTASE.4; 1.
Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;
Cholesterol biosynthesis; NADP; Peroxisome.
DOMAIN      1 363 MEMBRANE-BOUND.
DOMAIN      364 466 LINKER.
DOMAIN      467 948 CATALYTIC.
TRANSMEM    9 25 POTENTIAL.
TRANSMEM    55 71 POTENTIAL.
TRANSMEM    96 112 POTENTIAL.
TRANSMEM    124 140 POTENTIAL.
TRANSMEM    207 223 POTENTIAL.
TRANSMEM    286 302 POTENTIAL.
TRANSMEM    347 363 POTENTIAL.
ACT_SITE    567 567 BY SIMILARITY.
ACT_SITE    777 777 BY SIMILARITY.
ACT_SITE    869 869 GENERAL BASE (BY SIMILARITY).
SEQUENCE    948 AA; 107044 MW; CD5B9B84776371BF CRC64;

```

```
DR PIR: A35133; A35133.
DR Subtilisin; BG10485; comGC.
DR InterPro: IPR001120; Prok_N_methyltn.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Transport; Methylation; Transmembrane; Complete proteome.
FT CHAIN 1 5 BY SIMILARITY.
FT CHAIN 6 98 COMG OPERON PROTEIN 3.
FT TRANSMEM 6 26 POTENTIAL.
FT MOD_RES 6 6 METHYLATION (BY SIMILARITY).
FT DISULFID 41 81 PROBABLE.
SO SEQUENCE 98 AA; 10850 MW; 17B8152CAFE2F4C9 CRC64;

Query Match 45.5%; Score 40; DM 1; Length 98;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Caps 0;

OY 1 DSVCPCKYI 10
DB 78 DAVCPNGKRI 87

RESULT 13
ST5B_PIG STANDARD; PRT; 787 AA.
AC QRTU20;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Signal transducer and activator of transcription 5B.
GN ST5B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Mammary gland;
KA Palin M.F., Beaudry D., Roberge C., Farmer C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION AND
CC ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND
CC ACTIVATES PRL-INDUCED TRANSCRIPTION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY
CC MEMBER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in
CC response to phosphorylation (By similarity).
CC -1- PTM: TYROSINE PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC
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CC
CC EMBL: AF135123; AAD46164.1;
CC HSSP: P42227; IBG1.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001217; STAT.
CC Pfam: PF00017; SH2; 1.
CC Pfam: PF01017; STAT; 1.
CC Pfam: PF02864; STAT_bind; 1.
CC Pfam: PF02865; STAT_prot; 1.
CC SMART: SM00252; SH2; 1.
CC PROSITE: PS50001; SH2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
CC Phosphorylation; SH2 domain; Polymorphism.
CC DOMAIN 589 686
FT VARIANT 197 197 C -> R.
FT VARIANT 457 457 F -> S.
FT VARIANT 711 711 F -> L.
FT VARIANT 794 794 T -> I.
FT MOD_RES 699 699 P -> L.
FT SEQUENCE 153 153 PHOSPHORYLATION (BY JAK) (BY SIMILARITY).

DR PIR: A35133; A35133.
DR Subtilisin; BG10485; comGC.
DR InterPro: IPR001120; Prok_N_methyltn.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Transport; Methylation; Transmembrane; Complete proteome.
FT CHAIN 1 5 BY SIMILARITY.
FT CHAIN 6 98 COMG OPERON PROTEIN 3.
FT TRANSMEM 6 26 POTENTIAL.
FT MOD_RES 6 6 METHYLATION (BY SIMILARITY).
FT DISULFID 41 81 PROBABLE.
SO SEQUENCE 98 AA; 10850 MW; 17B8152CAFE2F4C9 CRC64;

Query Match 44.9%; Score 39.5; DB 1; Length 787;
Best Local Similarity 61.5%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Caps 1;

OY 2 SVCPOGKY-IHQ 13
DB 733 AVCPOAHYSYIQ 745

RESULT 14
ST5A_PIG STANDARD; PRT; 799 AA.
AC QRTU21;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Signal transducer and activator of transcription 5A.
GN ST5A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Mammary gland;
KA Palin M.F., Beaudry D., Roberge C., Farmer C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION AND
CC ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND
CC ACTIVATES PRL-INDUCED TRANSCRIPTION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY
CC MEMBER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in
CC response to phosphorylation (By similarity).
CC -1- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2, IL-3, IL-7, IL-
CC 15, GM-CSF, GROWTH HORMONE, PROLACTIN, ERYTHROPOIETIN AND
CC THROMBOPOIETIN. TYROSINE PHOSPHORYLATION IS REQUIRED FOR DNA-
CC BINDING ACTIVITY AND DIMERIZATION. SERINE PHOSPHORYLATION IS ALSO
CC REQUIRED FOR MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC
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CC
CC EMBL: AF135122; AAD46163.1;
CC HSSP: P42227; IBG1.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001217; STAT.
CC Pfam: PF00017; SH2; 1.
CC Pfam: PF01017; STAT; 1.
CC Pfam: PF02864; STAT_bind; 1.
CC Pfam: PF02865; STAT_prot; 1.
CC SMART: SM00252; SH2; 1.
CC PROSITE: PS50001; SH2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
CC Phosphorylation; SH2 domain; Polymorphism.
CC DOMAIN 589 686
FT VARIANT 197 197 C -> R.
FT VARIANT 457 457 F -> S.
FT VARIANT 711 711 F -> L.
FT VARIANT 794 794 T -> I.
FT MOD_RES 699 699 P -> L.
FT SEQUENCE 799 AA; 90954 MW; 310C123A8B624FF4 CRC64;
```

Query Match 44.9%; Score 39.5; DB 1; Length 799;
Best Local Similarity 61.5%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Search completed: May 21, 2003, 18:26:10
Job time : 13 secs

OY 2 SVCPOGKY-IHPQ 13
DB 733 AVCPOAHYSIYPQ 745

RESULT 15

OID3_TRIHA STANDARD; PRT: 143 AA.
AC P52755;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell wall protein QID3 precursor.
GN QID3.
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 2413;
RX MEDLINE=94166756; PubMed=8121402;
RA Lora J.M., de la Cruz J., Benitez T., Llobell A., Pintor-Toro J.A.;
RT "A putative catabolite-repressed cell wall protein from the
mycoparasitic fungus Trichoderma harzianum.";
RL Mol. Gen. Genet. 242:461-466(1994)
CC -!- FUNCTION: CONTRIBUTES TO SURFACE HYDROPHOBICITY, WHICH IS
CC IMPORTANT FOR PROCESSES SUCH AS ASSOCIATION OF HYPHAE IN
CC REPRODUCTIVE STRUCTURES, DISPERSAL OF AERIAL SPORES AND ADHESION
CC OF PATHOGENS TO HOST STRUCTURES.
CC -!- SURCELLULAR LOCATION: CELL WALL PROTEIN (POTENTIAL).
CC -!- INDUCTION: By carbon starvation.
CC -!- SIMILARITY: BELONGS TO THE CERATO-ULMIN HYDROPHOBIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X71913; CAA50728.1; .
KW Cell wall; Signal; Repeat.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 143 CELL WALL PROTEIN QID3.
FT DOMAIN 22 27 POLY-PRO.
FT DOMAIN 31 34 POLY-PRO.
FT DOMAIN 41 64 10 X 2 AA REPEAT OF N-G.
FT REPEAT 41 42 1.
FT REPEAT 43 44 2.
FT REPEAT 47 48 3.
FT REPEAT 49 50 4.
FT REPEAT 51 52 5.
FT REPEAT 53 54 6.
FT REPEAT 55 56 7.
FT REPEAT 59 60 8.
FT REPEAT 61 62 9.
FT REPEAT 63 64 10.
SQ SEQUENCE 143 AA; 14020 MW; 4948F9B08ACE30DF CFC64;

Query Match 44.3%; Score 39; DB 1; Length 143;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 SVCPOGKYIHPQ 13
DB 72 ALCPAGLYSNPQ 83

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:21:12 : Search time 84 Seconds
(without alignments)
39.247 Million cell updates/sec

Title: US-10-036-434-1

Perfect score: 88
Sequence: 1 DSVCPQCKYIHPOXNS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organellae.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_invertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacterioph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	85.2	17	4 Q9UCA4	Q9UCA4 homo sapien
2	72	81.8	189	6 Q95185	Q95185 felis silve
3	72	81.8	446	6 Q95ND3	Q95ND3 felis silve
4	68	77.3	189	6 Q95330	Q95330 canis famil
5	47	53.4	81	12 Q8QNK0	Q8QNK0 ectocarpus
6	46	52.3	89	3 P79072	P79072 trichoderma
7	46	52.3	356	10 Q9PHK2	Q9PHK2 arabidopsis
8	46	52.3	649	4 Q9NT29	Q9NT29 homo sapien
9	46	52.3	1400	4 Q9UP57	Q9UP57 homo sapien
10	45	51.1	98	4 Q963F5	Q963F5 homo sapien
11	45	51.1	198	10 Q9C9R5	Q9C9R5 arabidopsis
12	45	51.1	958	4 Q8WIT2	Q8WIT2 homo sapien
13	45	51.1	1043	5 Q17644	Q17644 caenorhabdi
14	45	51.1	3034	11 Q35161	Q35161 mus musculu
15	43	48.9	416	16 Q57456	Q57456 synecocyst
16	43	48.9	569	2 Q9AJB2	Q9AJB2 ruminococcu

17	43	48.9	726	2 Q9AJB3	Q9AJB3 ruminococcu
18	42	47.7	243	5 Q01309	Q01309 botryllus s
19	42	47.7	258	16 Q9KTJ8	Q9KTJ8 vibrio chol
20	42	47.7	325	2 Q9L6U1	Q9L6U1 xanthomonas
21	42	47.7	337	10 Q9LPE6	Q9LPE6 arabidopsis
22	42	47.7	425	10 Q8VXZ9	Q8VXZ9 arabidopsis
23	42	47.7	426	10 Q8W254	Q8W254 arabidopsis
24	42	47.7	745	13 Q91701	Q91701 xenopus lae
25	42	47.7	747	13 Q91900	Q91900 xenopus lae
26	42	47.7	1537	4 Q8WY29	Q8WY29 homo sapien
27	42	47.7	4599	4 Q9NZR2	Q9NZR2 homo sapien
28	41	46.6	145	16 Q26032	Q26032 helicobacte
29	41	46.6	243	5 Q01310	Q01310 botryllus s
30	41	46.6	266	10 Q9AR91	Q9AR91 medicago tr
31	41	46.6	467	5 Q15993	Q15993 penaeus jap
32	41	46.6	662	12 Q9QU30	Q9QU30 ttv-like m
33	41	46.6	663	12 Q9QU33	Q9QU33 ttv-like m
34	41	46.6	698	5 Q9UAC0	Q9UAC0 leishmania
35	41	46.6	700	5 Q9UAB9	Q9UAB9 leishmania
36	41	46.6	704	5 Q9UAC2	Q9UAC2 leishmania
37	41	46.6	743	13 Q9YGE7	Q9YGE7 oncorhynch
38	40.5	46.0	680	13 Q8QGJ3	Q8QGJ3 fundulus he
39	40	45.5	108	16 Q9JUN6	Q9JUN6 neisseria m
40	40	45.5	177	5 Q9VXT3	Q9VXT3 drosophila
41	40	45.5	224	10 Q9M3U7	Q9M3U7 medicago tr
42	40	45.5	242	10 Q9LDJ8	Q9LDJ8 medicago tr
43	40	45.5	242	10 Q9M3U6	Q9M3U6 medicago tr
44	40	45.5	257	16 Q9BWT6	Q9BWT6 rhizobium l
45	40	45.5	276	16 Q9K8N3	Q9K8N3 bacillus ha

ALIGNMENTS

RESULT 1					
Q9UCA4					
ID	Q9UCA4	PRELIMINARY;	PRT;	17 AA.	
AC	Q9UCA4;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)				
DE	Tumor necrosis factor inhibitor I (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=94286045; PubMed=8015639;				
RA	Suzuki J., Tomizawa S., Arai H., Seki Y., Maruyama K., Kuroume T.;				
RT	"Purification of two types of TNF inhibitors in the urine of the				
RT	patient with chronic glomerulonephritis.";				
RL	Nephron 66:386-390(1994).				
SO	SEQUENCE 17 AA; 1903 MW; D4418485E6981B28 CRC64;				

Query Match	85.2%	Score 75;	DB 4;	Length 17;
Best Local Similarity	93.8%	Pred. No. 4.7e-06;		
Matches 15;	Conservative	0;	Mismatches 1;	Indels 0;
QY	1 DSVCPQCKYIHPOXNS 16			
DB	1 DSVCPQCKYIHPOXNS 16			
III				
RESULT 2				
Q95185				
ID	Q95185	PRELIMINARY;	PRT;	189 AA.
AC	Q95185;			
DT	01-FEB-1997 (TrEMBLrel. 02, Created)			
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Tumor necrosis factor receptor p60 (Fragment).			
GN	TNFR-1.			

```
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A..
RA Duthie S., Nasir L., Eckersall P.D.;
RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT partial cds.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U72344; AB050891; -.
DR HSSP: P19438; IEXT.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBEOCE809U7DBE CRC64;

Query Match 81.8%; Score 72; DB 6; Length 189;
Best Local Similarity 92.3%; Pred. No. 0.00018;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CPOGKYIHPQXNS 16
DB 44 CPOGKYIHPQXNS 56
|||||
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RESULT 3
Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tumor necrosis factor type 1.
GN TNFR 1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR 1) and expression of TNFR 1 and TNFR II in various disease in
RT cats.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB051103; BAB55455.1; -.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD311DD8A74AA CRC64;

Query Match 81.8%; Score 72; DB 6; Length 446;
Best Local Similarity 92.3%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CPOGKYIHPQXNS 16
DB 44 CPOGKYIHPQXNS 16
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|||||

RESULT 4
Q97530 PRELIMINARY; PRT; 189 AA.
AC Q97530;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21109092; PubMed=11182158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
DR EMBL: AF013955; RAD01516.1; -.
DR HSSP: P19438; ITNR.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;

Query Match 77.3%; Score 68; DB 6; Length 189;
Best Local Similarity 78.6%; Pred. No. 0.00085;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VCPQSKYIHPQXNS 16
DB 43 LCPOGKYIHPQXNS 56
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|||||

RESULT 5
Q8ONKO PRELIMINARY; PRT; 81 AA.
AC Q8ONKO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE EsV-1-73.
OS Ectocarpus siliculosus virus.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
OX NCBI_TaxID=37665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ESV-1;
RA Delarouge N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W.;
RT "The complete nucleotide sequence of the Ectocarpus siliculosus virus
RT genome.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF204951; AAK14496.1; -.
SQ SEQUENCE 81 AA; 9336 MW; 29DF951525499EEC CRC64;

Query Match 53.4%; Score 47; DB 12; Length 81;
Best Local Similarity 58.3%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSVCPQSKYIHP 12
DB 58 DHFCPAGKVVP 69
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Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 VCPCKGYTHPQ 13
II:II:II:II:II
DB 5 VCEKCKYTHPQ 15

RESULT 8
Q9NT29 PRELIMINARY; PRT; 649 AA.
AC Q9NT29;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 68.7 kDa protein (Fragment).
CN DKF2P434D098.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.

RC TISSUE-TESTIS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wilmann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL137564; CAB70815.1;
DR HSSP; P00519; 1AB2.
DR InterPro; IPR000050; PID_domain.
DR InterPro; IPR002965; Prich_extensn.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRODOM; PD000093; SH2; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 649 AA; 68680 MW; 090C0BF86D9044BF CRC64;

Query Match 52.3%; Score 45; DB 4; Length 649;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 SVCPOGKYHP 12
II:II:II:II:II
DB 13 TMCPEGYHP 23

RESULT 9
Q9UPS7 PRELIMINARY; PRT; 1400 AA.
AC Q9UPS7; Q96P25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIAA1075 protein (Tensin2) (Fragment).
CN KIAA1075.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
RX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.

RESULT 6
P79072 PRELIMINARY; PRT; 89 AA.
AC P79072;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Spore-related hydrophobin SRH1 precursor.
CN SRH1.
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; mitosporic hyphae; Trichoderma.
OX NCBI_TaxID=5344;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=PI; TISSUE-MYCELIUM;
RX MEDLINE=97480703; PubMed=9339348;
RA Munoz G., Nakari-Setälä T., Agosin E., Penttilä M.;
RT "Hydrophobin gene srh1, expressed during sporulation of the biocontrol
agent Trichoderma harzianum";
RL Curr. Genet. 32:225-230(1997).
CC 1- FUNCTION: RESPONSIBLE FOR SPORE HYDROPHOBICITY AND PROTECTION.
CC 1- SUBCELLULAR LOCATION: PROBABLY ON SPORE WALL.
CC 1- DEVELOPMENTAL STAGE: EXPRESSED IN SPORULATING AERIAL AND SUBMERGED
CC CULTURES AND IN VEGETATIVE AERIAL HYPHAE.
CC 1- INDUCTION: BY C AND N STARVATION.
CC 1- PTM: FOUR DISULFIDE BONDS MAY BE PRESENT (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE CERATO-ULMIN SUBFAMILY OF HYDROPHOBINS.
DR EMBL; Y11841; CA472339.1;
KW Signal; Cell wall.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 89 SPORE-RELATED HYDROPHOBIN SRH1.
SQ SEQUENCE 89 AA; 9028 MW; 8A312E85CD664585 CRC64;

Query Match 52.3%; Score 46; DB 3; Length 89;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 SVCPOGKYHPQ 13
II:II:II:II:II
DB 18 SVCPLNGLYSNPQ 29

RESULT 7
Q9FHK2 PRELIMINARY; PRT; 356 AA.
AC Q9FHK2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Emb|CAB86478.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
features of the regions of 3,076,755 bp covered by sixty P1 and TAC
clones";
RT DNA Res. 7:31-63(2000).
RL EMBL; AB018112; BAB10974.1;
DR EMBL; AB026643; BAB10974.1; JOINED.
SQ SEQUENCE 356 AA; 41104 MW; D8BCC361D7F12325 CRC64;

Query Match 52.3%; Score 46; DB 10; Length 356;

```

RL  DNA Res. 6:197-205(1999).
RN  [2]
RP  SEQUENCE OF 116-1400 FROM N.A.
RA  Chen H., Lo S.H.
RT  "Molecular characterization of human tensin2 cDNA sequence."
RL  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL: AB028998; BAA83027.1; -
DR  EMBL: AF417490; AAL14641.1; -
DR  HSSP: P00519; IAB2.
DR  InterPro: IPR002219; DAG_PE-bind.
DR  InterPro: IPR000340; DS_phosphatase.
DR  InterPro: IPR000050; PID_domain.
DR  InterPro: IPR000980; SH2.
DR  Pfam: PF00130; DAG_PE-bind; 1.
DR  Pfam: PF00017; SH2; 1.
DR  PRINTS: PR00401; SH2DOMAIN.
DR  ProDom: PD000093; SH2; 1.
DR  SMART: SM00109; C1; 1.
DR  SMART: SM00462; PTB; 1.
DR  SMART: SM00012; PTPC_DSpc; 1.
DR  SMART: SM00252; SH2; 1.
DR  PROSITE: PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR  PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
DR  PROSITE: PS50001; SH2; 1.
FT  NON_TER 1 1
SO  SEQUENCE 1400 AA; 151628 MW; 555D976125A946D7 CRC64;

Query Match 52.3%; Score 46; DB 4; Length 1400;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Caps 0;

QY  2 SVCPQGYIHP 12
Db  762 TMCPEGRYGH 772

RESULT 10
Q96SF5
ID  Q96SF5 PRELIMINARY; PRT; 98 AA.
AC  Q96SF5;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  BA55SG22.1 (KIAA1008 protein) (fragment).
GN  BA55SG22.1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Blakesy S.;
RI  Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RL  EMBL: AL391384; CAC39623.1; -
FT  NON_TER 98 98
SO  SEQUENCE 98 AA; 10403 MW; D5FF25DD73ACF578 CRC64;

Query Match 51.1%; Score 45; DB 4; Length 98;
Best Local Similarity 57.1%; Pred. No. 3.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Caps 0;

QY  2 SVCPQGYIHPQXN 15
Db  58 SVCPQPHYLLPDN 71

RESULT 11
Q9C9R5
ID  Q9C9R5 PRELIMINARY; PRT; 198 AA.
AC  Q9C9R5;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE  DNA Res. 6:197-205(1999).
RN  [2]
RP  SEQUENCE OF 116-1400 FROM N.A.
RA  Chen H., Lo S.H.
RT  "Molecular characterization of human tensin2 cDNA sequence."
RL  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL: AB028998; BAA83027.1; -
DR  EMBL: AF417490; AAL14641.1; -
DR  HSSP: P00519; IAB2.
DR  InterPro: IPR002219; DAG_PE-bind.
DR  InterPro: IPR000340; DS_phosphatase.
DR  InterPro: IPR000050; PID_domain.
DR  InterPro: IPR000980; SH2.
DR  Pfam: PF00130; DAG_PE-bind; 1.
DR  Pfam: PF00017; SH2; 1.
DR  PRINTS: PR00401; SH2DOMAIN.
DR  ProDom: PD000093; SH2; 1.
DR  SMART: SM00109; C1; 1.
DR  SMART: SM00462; PTB; 1.
DR  SMART: SM00012; PTPC_DSpc; 1.
DR  SMART: SM00252; SH2; 1.
DR  PROSITE: PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR  PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
DR  PROSITE: PS50001; SH2; 1.
FT  NON_TER 1 1
SO  SEQUENCE 1400 AA; 151628 MW; 555D976125A946D7 CRC64;

Query Match 52.3%; Score 46; DB 4; Length 1400;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Caps 0;

QY  2 SVCPQGYIHP 12
Db  762 TMCPEGRYGH 772

RESULT 10
Q96SF5
ID  Q96SF5 PRELIMINARY; PRT; 98 AA.
AC  Q96SF5;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  BA55SG22.1 (KIAA1008 protein) (fragment).
GN  BA55SG22.1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Blakesy S.;
RI  Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RL  EMBL: AL391384; CAC39623.1; -
FT  NON_TER 98 98
SO  SEQUENCE 98 AA; 10403 MW; D5FF25DD73ACF578 CRC64;

Query Match 51.1%; Score 45; DB 4; Length 98;
Best Local Similarity 57.1%; Pred. No. 3.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Caps 0;

QY  2 SVCPQGYIHPQXN 15
Db  58 SVCPQPHYLLPDN 71

RESULT 11
Q9C9R5
ID  Q9C9R5 PRELIMINARY; PRT; 198 AA.
AC  Q9C9R5;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE  Hypothetical 22.4 kDa protein.
RN  [1]
RP  SEQUENCE FROM N.A.
RA  STRAIN-CV, COLUMBIA;
RL  MEDLINE=21016719; PubMed=11130712;
RA  Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA  White O., Alonso J., Araujo R., Bowman C.L., Brooks S.Y.,
RA  Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA  Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA  Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA  Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA  Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA  Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA  Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-p.,
RA  Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA  Millitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA  Paj G., Peterson J., Pham P.K., Kizzo M., Rooney T., Southwick A.M.,
RA  Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Town C.D.,
RA  Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA  Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA  Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT  "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT  thaliana";
RL  Nature 408:816-820(2000).
DR  EMBL: AC012680; AAG52095.1; -
DR  InterPro: IPR000345; Cytochrome_c; UNKNOWN_1.
DR  PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KW  Hypothetical protein.
SQ  SEQUENCE 198 AA; 22396 MW; 8B001E9B24685D53 CRC64;

Query Match 51.1%; Score 45; DB 10; Length 198;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Caps 0;

QY  3 VCPQGYIHPQXNS 16
Db  170 VCPNCKRPMIPDHNS 183

RESULT 12
Q8WWI2
ID  Q8WWI2 PRELIMINARY; PRT; 958 AA.
AC  Q8WWI2;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  KIAA1008 protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  TISSUE-BRAIN, AND PERIPHERAL BLOOD LEUKOCYTES;
RA  Rozenblum E., Vaheristo P., Sandberg T., Bergthorsson J.,
RA  Syrjäsakoski K., Weaver D., Haraldsson K., Johannsdottir H.K.,
RA  Vehmanen P., Nigam S., Goldberger N., Robbins C., Pak E., Dutra A.,
RA  Gillanders E., Stephan D., Bailey-Wilson J., Joo S., Kainu T.,
RA  Arason A., Barkardottir R.B., Nevanlinna H., Borg A., Kallioniemi O.;
RT  "A genomic map of a 6 Mb region at 13q12-q22 implicated in cancer
RT  development: identification and characterization of candidate genes."
RL  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR  EMBL: AF330044; AAL37479.1; -
DR  InterPro: IPR001900; Ribonuclease_II.
DR  Pfam: PF00773; RNB; 1.
DR  PROSITE: PS01175; RIBONUCLEASE_II; UNKNOWN_1.
DR  SEQUENCE 958 AA; 108975 MW; 7ACB0A4612A8D9E4 CRC64;

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Query Match 51.1%; Score 45; DR 4; Length 958;
 Best Local Similarity 57.1%; Pred. No. 36;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 SVCPQCKYIHPQXN 15
 ||||| | | | |
 DB 58 SVCPQPHYLLPDPTN 71

RESULT 13
 O17644 PRELIMINARY; PRT; 1043 AA.
 AC O17644
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE C34F6.1 protein.
 GN C34F6.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
 OC Rhabditiidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA White S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 KN [2]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; 281479; CAB03944.1; -.
 DR HSSP; p10646; 1AD2.
 DR InterPro; IPK002223; Kunitz_BPTI.
 DR InterPro; IPK002899; WRI/EB.
 DR Pfam; PF00014; Kunitz_BPTI; 8.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 8.
 DR SMART; SM00131; KU; 8.
 DR SMART; SM00289; WRI; 6.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 8.
 KW Serine protease inhibitor.
 FT SIGNAL 1 26
 FT CHAIN 27 3034
 SQ SEQUENCE 1043 AA; 115537 MW; F25F5FE87FA1FAA5 CRC64;

Query Match 51.1%; Score 45; DB 5; Length 1043;
 Best Local Similarity 63.6%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DSVCPQCKYIHP 11
 ||:|| | | | |
 DB 322 DSMCPNGYCH 332

RESULT 14
 O35161 PRELIMINARY; PRT; 3034 AA.
 ID O35161
 AC O35161
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Seven-pass transmembrane receptor precursor.
 GN CELSR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 KC STRAIN=C57/BL6; TISSUE=BRAIN;
 RX MEDLINE=97480720; PubMed=9339365;

RA Hadjantonakis A.K., Sheward W.J., Harnar A.J., de Galan L.,
 RA Hoovers J.M., Little P.F.;
 RT "Celsr1, a neural-specific gene encoding an unusual seven-pass
 transmembrane receptor, maps to mouse chromosome 15 and human
 chromosome 22qter.";
 RL Genomics 45:97-104(1997).
 CC -!- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
 DR EMBL; AF031572; AAC68836.1; -.
 DR HSSP; P00749; IURK.
 DR MGD; MGI:1100883; Celsr1.
 DR InterPro; IPK00152; Asx_hydroxyl.
 DR InterPro; IPK002126; Cadherin.
 DR InterPro; IPK000561; EGF-like.
 DR InterPro; IPK000832; GPCR_secretin.
 DR InterPro; IPK001879; hormn_receptor.
 DR InterPro; IPK002049; laminin_EGF.
 DR InterPro; IPK001791; Laminin-G.
 DR InterPro; IPK00203; PKD_cys_rich.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF00028; cadherin; 9.
 DR Pfam; PF00008; EGF; 6.
 DR Pfam; PF01825; GPS; 1.
 DR Pfam; PF02793; HRM; 1.
 DR Pfam; PF00053; laminin_EGF; 1.
 DR Pfam; PF00054; laminin-G; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00112; CA; 9.
 DR SMART; SM00180; EGF_Lam; 1.
 DR SMART; SM00001; EGF_Like; 6.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00008; Hormr; 1.
 DR SMART; SM00282; Lamg; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
 DR PROSITE; PS00232; CADHERIN_1; 6.
 DR PROSITE; PS50268; CADHERIN_2; 9.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_6.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 KW Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein;
 KW Receptor; Signal; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 3034
 SQ SEQUENCE 3034 AA; 330477 MW; EFF38180AF3ED8A8 CRC64;

Query Match 51.1%; Score 45; DB 11; Length 3034;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 VCPQCKYIHP 12
 ||| | | | |
 DB 1444 VCPPEYEHHP 1453

RESULT 15
 Q57456 PRELIMINARY; PRT; 416 AA.
 ID Q57456
 AC Q57456
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein slr0351.
 GN SLR0351.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RX Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

RA Suglura M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. 1. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cassier-Chauvat C., Poncellet M., Viljoing S., Chauvat F.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D64000; BAA10162.1; -;
 DR EMBL: U38915; AAB72122.1; -;
 DR InterPro: IPR001091; CMA_Mettransf.
 DR InterPro: IPR003788; DUF185.
 DR Pfam: PF02636; DUF185; 1.
 DR PROSITE: PS00093; N4_MTASE; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 416 AA; 46828 MW; 43DA24914AA30D61 CRC64;

Query Match 48.9%; Score 43; DB 16; Length 416;
 Best Local Similarity 77.8%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 POGKYHPQ 13
 I I I I I I
 DB 274 PAGKYHPQ 282

Search completed: May 21, 2003, 18:27:43
 Job time : 87 secs